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Doctoral Dissertation

Development of Chemical Tactics
to Study Fundamental Aspects of Pathogenic
Factors Found in Neurodegenerative Diseases

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2019

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A dissertation submitted to the Graduate School of UNIST
in partial fulfillment of the requirements
for the degree of Doctor of Philosophy of Science

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March 29, 2019

Approved by



Advisor

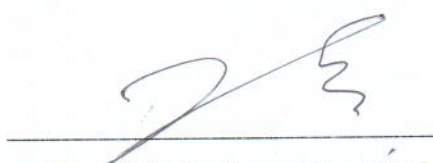
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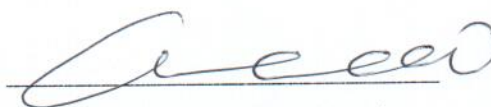
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Abstract

Amyloidogenic peptides are considered central pathological factors in neurodegenerative diseases; however, their roles in the pathologies of the diseases have not been fully understood. Amyloidogenic peptides have indicated their multiple faces on formation, aggregation, and accumulation that portray the complexity of the intrinsically disordered protein stemming from their convoluted structure and heterogeneous nature. Although the latest research suggests oligomeric forms of amyloidogenic peptides as toxic species towards neurodegeneration, their direct involvements in the pathologies and the corresponding mechanistic details remain rudimentary. Therefore, novel chemical approaches to modify amyloidogenic peptides at the molecular level would be useful in advancing our comprehension of those aspects and the subject.

In Chapter 1, we briefly introduce outline and discuss possible therapeutic targets in Alzheimer's disease. In Chapter 2, the design of an Ir(III) complex, **Ir-1**, is described as a chemical tool for oxidizing amyloidogenic peptides upon photoactivation and subsequently modulating their aggregation pathways. Biochemical and biophysical investigations illuminate that the oxidation of representative amyloidogenic peptides [i.e., amyloid- β ($A\beta$), α -synuclein, and human islet amyloid polypeptide] is promoted by light-activated **Ir-1**, which can alter the conformations and aggregation pathways of the peptides. In Chapter 3, effective chemical strategies for modifications of $A\beta$ peptides implemented by a single Ir(III) complex are illustrated. Such peptide variations can be achieved by our rationally designed Ir(III) complexes leading to the significant modulation of the aggregation pathways of $A\beta_{40}$ and $A\beta_{42}$ as well as the production of toxic $A\beta$ species.

Amyloidogenic peptides can coordinate to metal ions, including Zn(II), which can subsequently affect the peptides' aggregation and toxicity, leading to neurodegeneration. Unfortunately, the detection of metal–amyloidogenic peptide complexation has been very challenging. In Chapter 4, we report the development and utilization of a probe (**A-1**) capable of monitoring metal– $A\beta$ complexation based on Förster resonance energy transfer (FRET). Moreover, as the FRET signal of Zn(II)-added **A-1** is drastically changed when the interaction between Zn(II) and **A-1** is disrupted, the Zn(II)-treated probe can be used for screening a chemical library to determine effective inhibitors against metal– $A\beta$ interaction.

Overall, we demonstrate chemical tactics for modifications of amyloidogenic peptides in an effective and manageable manner utilizing the coordination capacities and/or photophysical properties of chemical reagents. Our approaches will provide the foundation for developing effective and efficient methods for elucidating fundamental properties of pathological factors at the molecular level and assisting in identifying therapeutic candidates against neurodegenerative disorders.

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Scheme 4.1. Synthetic routes to A-1.

List of Abbreviations

5Y	SH-SY5Y
A β	Amyloid- β
ABDA	9,10-Anthracenediyl-bis(methylene)dimalonic acid
Acetyl-CoA	Acetyl coenzyme A
ACh	Acetylcholine
AChE	Acetylcholinesterase
AChEIs	Acetylcholinesterase inhibitors
AD	Alzheimer's disease
AFM	Atomic force microscopy
ALS	Amyotrophic lateral sclerosis
ApoE	Apolipoprotein E
APP	Amyloid precursor protein
α -Syn	α -Synuclein
ATDs	Arrival time distributions
BACE1	β -Site APP cleaving enzyme
BAX	Bcl-2 associated X
BBB	Blood-brain barrier
Bcl-2	B-cell lymphoma 2
BuChE	Butyrylcholinesterase
cAMP	Cyclic adenosine monophosphate
CcO	Cytochrome c oxidase
CD	Circular dichroism spectroscopy
cdk5	Cyclin-dependent kinase-5
cGMP	Cyclic guanosine monophosphate
ChAT	Choline acetyltransferase
ChEIs	Cholinesterases inhibitors
ChEs	Cholinesterases
CNS	Central nervous system
COMMD1	COMM domain-containing protein 1
CP-MD simulation	Car-Parrinello molecular dynamics simulation
CREB	cAMP (cyclic adenosine monophosphate) response element binding
CSPs	Chemical shift perturbations
CTF α	C-terminal fragment α

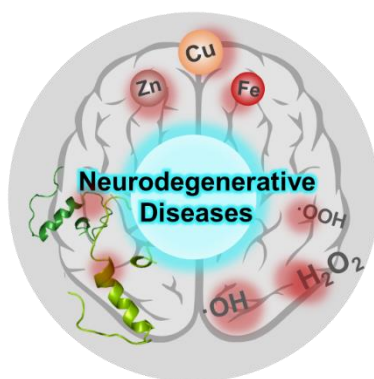
CypD	Cyclophilin D
DβM	Dopamine β monooxygenase
DCM	Dichloromethane
DIPEA	<i>N,N</i> -Diisopropylethylenediamine
DKK1	Dickkopf1
DMEM	Dulbecco modified eagle medium
DMF	<i>N,N</i> -Dimethylformamide
DMSO	Dimethyl sulfoxide
DMT1	Divalent metal-ion transporter-1
Dnap	1-Naphthylethylenediamine
DPBS	Dulbecco's phosphate-buffered saline
ECL	Enhanced chemiluminescence
EDTA	Ethylenediamine tetraacetic acid
EPR	Electron paramagnetic resonance spectroscopy
ER	Endoplasmic reticulum
ESI	Electrospray ionization
ESI-IM-MS	Electrospray ionization ion mobility mass spectrometry
ESI-MS	Electrospray ionization-mass spectrometry
Et ₂ O	Diethyl ether
EtOAc	Ethyl acetate
EXAFS	Extended X-ray absorption fine structure
FBS	Fetal bovine serum
FDA	Food and Drug Administration
FRET	Förster resonance energy transfer
FTD	Frontotemporal dementia
FTIR	Fourier-transform infrared spectroscopy
GABA	Aminobutyric acid
Gel/Western blot	Gel electrophoresis with Western blotting
GSK3	Glycogen synthase kinase 3
hAChE	Human acetylcholinesterase
HBTU	2-(1 <i>H</i> -Benzotriazol-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate
HDACs	Histone deacetylases
HEPES	4-(2-Hydroxyethyl)-1-piperazineethanesulfonic acid
HFIP	1,1,1,3,3,3-Hexafluoro-2-propanol
hIAPP	Human islet amyloid polypeptide
HOAt	1-Hydroxy-7-azabenzotriazole

HOBt	1-Hydroxy-benzotriazole
HPLC	High-performance liquid chromatography
HRMS	High-resolution mass spectrometry
ICT	Isothermal titration calorimetry
IM-MS	Ion mobility mass spectrometry
IRF	Instrument response function
JNK	c-Jun N-terminal kinase
K_d	Binding affinities
LTP	Long-term potentiation
MALDI-TOF	Matrix-assisted laser desorption/ionization time-of-flight
MAO	Monoamine oxidase
MAPs	Microtubule-associated proteins
MCI	Mild cognitive impairment
MEM	Minimum essential medium
MS	Mass spectrometry
MS ²	Tandem mass spectrometry
MTs	Metallothioneins
MTT	3-(4,5-Dimethyl-2-thiazolyl)-2,5-diphenyl-2 <i>H</i> -tetrazolium bromide
MWs	Molecular weights
N2a	Neuro-2a
NADPH oxidase	Nicotinamide adenine dinucleotide phosphate oxidase
Nap	<i>N</i> -Naphthylethylenediamine
NFTs	Neurofibrillary tangles
NMDA	<i>N</i> -Methyl-D-aspartate
NMDAR	<i>N</i> -Methyl-D-aspartate receptor
NMR	Nuclear magnetic resonance
PAS	Peripheral anionic site
PBS	Phosphate-buffered saline
PD	Parkinson's disease
PDB	Protein data bank
PDEIs	Phosphodiesterases inhibitors
PDEs	Phosphodiesterases
pGlu-A β	Pyroglutamate A β
PHFs	Paired helical filaments
PIPES	Piperazine- <i>N,N'</i> -bis(2-ethanesulfonic acid)
PLA2s	Phospholipase A2

PPAR γ	Peroxisome proliferator activator receptor γ
ptau	Hyperphosphorylated tau
ROS	Reactive oxygen species
S.E.M.	Standard errors of mean
sAPP α	Soluble amyloid precursor protein α
SAXS	Small-angle X-ray scattering
SDS	Sodium dodecyl sulfate
SFs	Straight filaments
SHG	Second harmonic generation
SOD	Superoxide dismutase
SOFAST-HMQC	2D band-selective optimized flip-angle short transient heteronuclear multiple quantum correlation
SPPS	Solid phase peptide synthesis
SPR	Surface plasmon resonance
SPs	Senile plaques
TBS	Tris-buffered saline
TCSPC	Timecorrelated single-photon counting
TEM	Transmission electron microscopy
TFA	Trifluoroacetic acid
ThT	Thioflavin-T
TLC	Thin layer chromatography
TNF	Tumor necrosis factor
TNF α	Tumor necrosis factor α
TRAIL	Tumor necrosis factor-related apoptosis-inducing ligand
TRAIL-R1	Tumor necrosis factor-related apoptosis-inducing ligand receptor 1
TRAIL-R2	Tumor necrosis factor-related apoptosis-inducing ligand receptor 2
Tris	Tris(hydroxymethyl)aminomethane
UV-vis	Ultraviolet-visible spectroscopy
XANES	X-ray absorption near edge structure
XAS	X-ray absorption spectroscopy
ZIPs	Zinc-regulated transporters, iron-regulated transporter-like proteins
ZnT	Zinc transporter
ZnT-3	Zinc transporter 3

Chapter 1.

Potential Pathological Factors in Alzheimer's Disease



This chapter was adapted from the publication [Savelieff M. G.;[†] Nam, G.;[†] Kang, J.;[†] Lee, H. J.; Lee, M.; Lim, M. H. *Chem. Rev.* **2019**, *119*, 1221–1322 ([†]equal contribution)]. I thank Professor Mi Hee Lim for her assistance and guidance throughout the writing of this manuscript.

1.1. Introduction

1.1.1. Neurodegenerative Diseases

Neurodegenerative diseases are characterized by the progressive loss of neuronal function. Despite a herculean effort, neurodegenerative diseases remain incurable. Research is revealing parallels between Alzheimer's disease (AD), the most prevalent form of dementia which accounts for ca. 60–80% of cases,¹ and other neurodegenerative diseases, including Parkinson's disease (PD)² and amyotrophic lateral sclerosis (ALS).³ As the global population ages and the number of individuals expected to develop neurodegenerative conditions increases, the search for an effective cure is becoming progressively more urgent.

An obstacle to drug discovery can in part be attributed to the multifactorial nature of most neurodegenerative illnesses. Although the specifics vary, several unifying threads that run through multiple neurodegenerative diseases have been identified. Proteopathy is one recurrent aspect, generally in the form of misfolded and aggregation-prone proteins and peptides, which may occur concurrently with defects in their clearance (Figure 1.1).^{4–6} AD is characterized by the deposition of senile plaques (SPs) and neurofibrillary tangles (NFTs), composed of the aggregates of amyloid- β (A β) and hyperphosphorylated tau (ptau), respectively.^{7,8}

Another prominent theme is metal ion dyshomeostasis in the brains of patients suffering from neurodegeneration.^{8–12} Under normal conditions, metal ions play several critical roles in the brain. They are cofactors for numerous enzymes with important catalytic activities (e.g., energy production) and serve as active participants in metal-dependent neurotransmission. Therefore, the proper regulation of metal ions is necessary for normal neuronal function. In neurodegenerative diseases, elevated or lowered levels as well as miscompartmentalization of metal ions are observed, leading to dysregulation of various downstream processes (Figure 1.1). One important consequence of metal ion dyshomeostasis [especially, redox-active Cu(I/II) and Fe(II/III)] is oxidative stress caused by reactive oxygen species (ROS) overproduced from Fenton-like reactions.^{10,13} In addition, metal ions are coordinated to amyloidogenic peptides (e.g., A β) and consequently modify their aggregation pathways.^{14–16} Other pathological features common to several neurodegenerative diseases include mitochondrial dysfunction,^{17–19} elevated oxidative stress,²⁰ defects in energy metabolism,^{21,22} aberrant axonal transport,^{23–25} and pervasive, sustained chronic inflammation (Figure 1.1).^{7,26} Thus, these pathological elements could trigger neuronal loss, alter neurotransmitter levels, and lower the capacity for signal transduction precipitating the progressive decline of cognitive and/or motor function and eventual death. Based on their inter-related roles in the pathogenesis of AD, metal ions and other inter-related pathological factors are implicated as important therapeutic targets in these diseases.

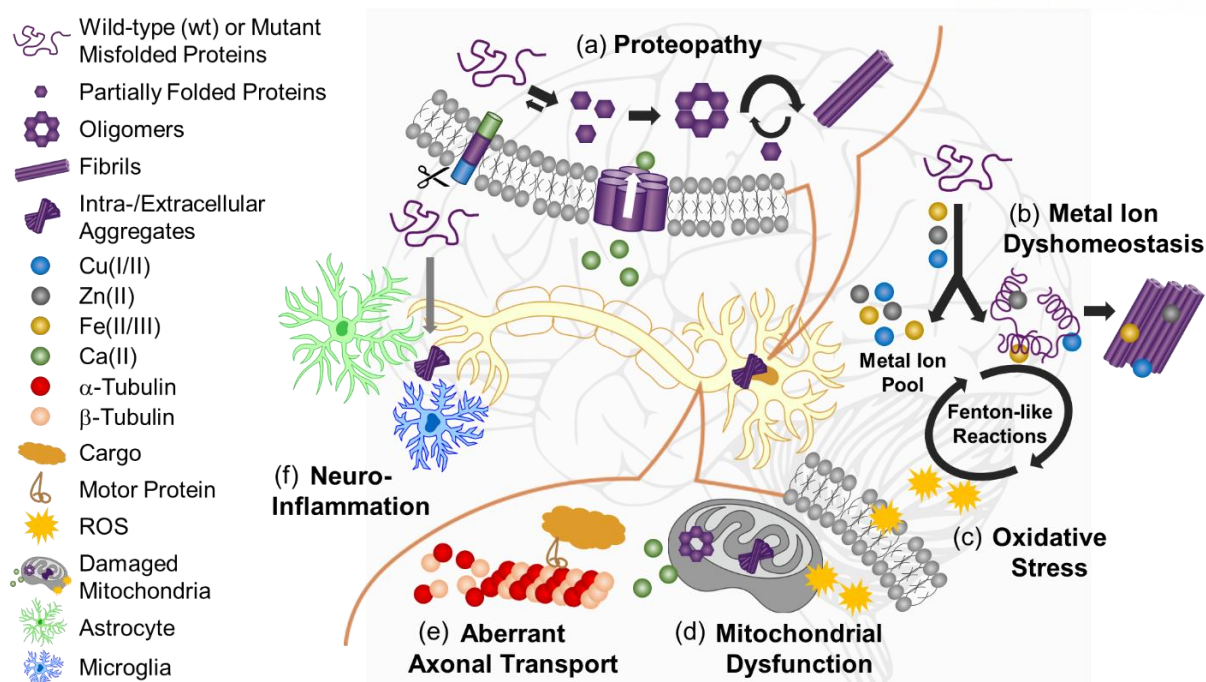


Figure 1.1. Multifactorial nature of neurodegenerative diseases. (a) Proteopathy of wild-type (wt) or mutant intra- or extracellular unfolded proteins/peptides. Unfolded monomers partially fold and aggregate into oligomers and fibrils. Oligomers may interact with various organelles (e.g., mitochondria) or cell membrane disrupting Ca(II) homeostasis and signaling. (b) Dyshomeostasis of metal ions that, depending on the disease, can bind to misfolded proteins/peptides affecting their aggregation or accumulate in the brain or spinal cord. (c) Elevated oxidative stress resulting from redox-active metal ions (i.e., Cu and Fe) via Fenton-like reactions or ROS escaping from damaged mitochondria. ROS can attack cellular proteins, nucleic acids, and lipids causing oxidative damage. (d) Mitochondrial dysfunction and defects in energy metabolism that can occur as a consequence of protein/peptide aggregates. (e) Aberrant axonal transport from hyperphosphorylated microtubule binding proteins, mutant tubulin proteins, or mutant motor proteins. (f) Pervasive, sustained chronic inflammation with reactive microglia and astrocytes as well as altered inflammatory signaling pathways.

Current therapeutic strategies are palliative and only manage symptoms for a short duration of time before cognitive abilities or motor function continue to degenerate. At present, for instance, widely administered treatments for AD are acetylcholinesterase inhibitors (AChEIs) which curb acetylcholine (ACh) degradation and thus maintain levels of neurotransmission.²⁷ This approach, however, invariably fails, and patients eventually succumb to deteriorating cognitive health. Development of efficacious drugs for neurodegenerative illnesses has been challenging because their precise etiology is not completely identified. A thorough comprehension of disease etiology would be beneficial to aid the discovery of effective therapeutics capable of targeting the root cause of neurodegenerative conditions in a disease-modifying manner. For example, the amyloid cascade hypothesis, the most widely held AD hypothesis, posits that the aggregates of $\text{A}\beta$ peptides, produced in the brain, are the primary cause of neurodegeneration.²⁸ Drugs altering the production, clearance, and aggregation of $\text{A}\beta$ have been developed and many have entered clinical trials. None, however, has successfully yielded significant

benefits, although some improvements were observed.²⁹ These failures have prompted a reexamination of the hypothesis suggesting that other factors, in addition to A β , may be mutually operating in neurodegeneration.³⁰ Another hurdle is timely treatment because neurodegeneration begins prior to disease onset and diagnosis. Intervening at this stage could halt further damage, but it may not be able to reverse the deterioration, which has already occurred. Compounded with these problems are challenges that come from treating a condition in the brain, which is generally nonregenerative, highly heterogeneous, and insulated by the blood-brain barrier (BBB).

Taken together, the multifaceted nature of neurodegenerative diseases suggests that an effective treatment might require a multipronged approach to simultaneously combat several pathological features. Towards this aim, numerous chemical tools capable of targeting and regulating pathological aspects of neurodegenerative disorders have been rationally designed, and studies have been conducted to assess their efficacies. This chapter describes possible therapeutic targets in AD-affected brains to advance our understanding of the etiology of the disease.

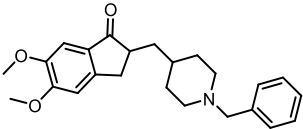
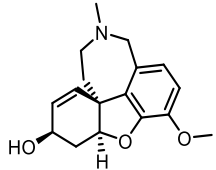
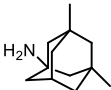
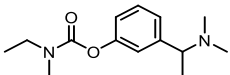
1.2. Alzheimer's Disease (AD)

In 1906, Alois Alzheimer introduced the world to a devastating disease widely known today as AD.³¹ AD is a progressive neurodegenerative disease responsible for 60 to 80% of dementia cases.^{1,32} According to the World Alzheimer Report, 47 million people worldwide were affected by AD in 2015 and this number is projected to increase to 75 million by 2030.¹ With the aging world population, the social and economic impact of AD is expected to rise significantly.³³ Since the discovery of AD, a great deal of progress has been made towards understanding its pathogenesis; however, we have yet to pinpoint its causative factors or fully elucidate its pathology. More importantly, there are no treatments for AD that can cure or halt its progression. Current AD therapies either temporarily relieve symptoms by inhibiting acetylcholinesterase (AChE) to maintain the levels of ACh and cholinergic transmission or regulating the activation of *N*-methyl-D-aspartate (NMDA) receptors. Five AD treatments approved by the Food and Drug Administration (FDA) are available to relieve the symptoms of AD (Table 1.1): (i) three AChE inhibitors (i.e., **donepezil**, **galantamine**, and **rivastigmine**); (ii) an NMDA receptor (NMDAR) antagonist (i.e., **memantine**); (iii) a mixture of **donepezil** and **memantine**. The imminent amplification of the socioeconomic impact of AD and the lack of an effective treatment illustrate the urgent necessity to identify the underlying AD pathogenesis.

Loss of short-term and long-term memory is the most widely recognized AD symptom. Throughout the progression of AD, patients manifest a general decline in mental ability: language and motor skills, sensory information processing, and memory formation and retrieval.³⁴ The anatomical hallmarks of AD include the shrinkage of the hippocampus and cortex.³⁵ Histopathologically, AD compromises SPs and NFTs composed primarily of A β and tau, respectively.^{28,36,37} Along with its proteopathy, metal ion dyshomeostasis, imbalance between the production and removal of ROS, and

loss of cholinergic transmission are also implicated in AD pathology. Several hypotheses have arisen in an attempt to identify the principal pathological factors in AD: (i) amyloid cascade hypothesis; (ii) tau hypothesis; (iii) metal ion hypothesis; (iv) oxidative stress hypothesis; (v) cholinergic hypothesis. Thus, therapeutics targeting singular pathological factors presented in these hypotheses have proven ineffective, inferring the intricate nature of AD pathogenesis. Consequently, the contemporary direction concerning AD etiopathology increasingly appreciates its complexity and has transitioned from focusing on individual pathological components to illuminating the interrelations among multiple pathological factors.

Table 1.1. Currently available AD treatments.

Generic Name ^a	Structure	Approved for	FDA Approved	Therapeutic Target ^b
Donepezil		All Stages	1996	AChE
Galantamine		Mild to Moderate	2001	AChE
Memantine		Moderate to Severe	2003	NMDAR
Rivastigmine		Mild to Moderate	2000	AChE and BuChE
Donepezil + Memantine		Moderate to Severe		

^a**Donepezil**, 2-[(1-benzylpiperidin-4-yl)methyl]-5,6-dimethoxy-2,3-dihydro-1H-inden-1-one; **galantamine**, (4a*S*,6*R*,8a*S*)-5,6,9,10,11,12-hexahydro-3-methoxy-11-methyl-4a*H*-[1]benzofuro[3a,3,2-*ef*][2]-benzazepin-6-ol; **memantine**, 3,5-dimethyl-tricyclo[3.3.1.1.3,7]decan-1-amine; **rivastigmine**, (*S*)-3-[1-(dimethylamino)ethyl]phenyl-*N*-ethyl-*N*-methylcarbamate. ^bAChE, acetylcholinesterase; BuChE, butyrylcholinesterase; NMDAR, *N*-methyl-D-aspartate receptor.

1.2.1. Amyloid- β (A β) and Tau

AD proteopathy is portrayed by two highly recognized AD hypotheses: the amyloid cascade and tau hypotheses. The amyloid cascade hypothesis posits that A β , a proteolytic product of amyloid precursor protein (APP), is the causative factor in the course of AD pathology.³⁶ Genetic studies support the pertinence of A β in the pathogenesis of AD. Numerous AD genes are shown to influence A β pathology (e.g. *APOE*, *APP*, *PSEN1*, and *PSEN2*).³⁸ A common polymorphism, $\epsilon 4$, within *APOE* is reportedly associated with the late onset of AD. This mutation is characterized by elevated A β aggregation and

reduced A β clearance.^{39,40} Genetic variants in APP are connected with early onset familial AD.⁴¹ According to an AD mutation database, 51 APP gene mutations are believed to be linked to the increased A β_{42} :A β_{40} ratio as well as the production and aggregation of A β leading to AD.^{38,41} *PSEN1* and *PSEN2* mutations are indicated to be involved in the pathology of AD with 219 and 16 variants identified, respectively.⁴¹ Genetic mutations to *PSEN1* and *PSEN2* are shown to enhance the A β_{42} :A β_{40} ratio.³⁸

Responsible for the production of A β , APP processing can be categorized into nonamyloidogenic and amyloidogenic pathways.^{42–44} In nonamyloidogenic APP processing, the soluble APP α (sAPP α) and the C-terminal fragment α (CTF α) are formed by α -secretase cleavage.^{42–44} Subsequent cleavage of CTF α by γ -secretase results in the generation of p3, a nonamyloidogenic peptide. Amyloidogenic APP processing is initiated by β -secretase cleavage [e.g., β -site APP cleaving enzyme (BACE1)] producing sAPP β and CTF β .^{42–44} The generated CTF β is then cleaved by γ -secretase at multiple sites within the transmembrane domain, producing a range of A β monomers with 38 to 43 amino acid residues.^{42–45}

A β peptides possess a propensity to aggregate, which is a subject of intensive research. As an intrinsically disordered protein, A β lacks stabilized secondary or tertiary structures; however, it can exist in partially folded states depending on genetic mutations and external factors (e.g., pH, temperature, peptide concentration, and intermolecular interactions).⁴⁶ During on-pathway aggregation, composed of a nucleation phase followed by an elongation phase, monomeric A β species oligomerize through interactions between their self-recognition sites and hydrophobic C-terminal regions (Figure 1.2).⁴³ These metastable A β oligomers can further aggregate into protofibrils and fibrils which exhibit a β -sheet conformation.⁴⁶ Fibrils have been reported to contribute to the accumulation of A β oligomers through fragmentation and secondary nucleation.^{47,48} Due to their prominent presence in extracellular SPs, fibrils were initially thought to be responsible for the neurotoxicity found in AD.^{49,50} A lack of the correlation between SP load and the extent of neurodegeneration, however, led to the reevaluation of this notion.³⁶ Recent studies have supported an alternative concept of structured A β oligomers as potential toxic species.^{51–54} The toxic mechanisms of structured A β oligomers have been proposed to arise from their interactions with membranes and membrane receptors and the disruption of intracellular processes [e.g., induction of endoplasmic reticulum (ER) stress, lysosomal leakage, mitochondrial dysfunction, and signal interruption].^{46,55} Furthermore, A β transmissibility through a seeding effect has been suggested as a means to spread its toxicity, possibly to remote areas, through cell-to-cell transmission mechanisms.^{56,57} Overall, the amyloid cascade hypothesis presents potential therapeutic candidates that can directly influence the production, clearance, and aggregation of A β .

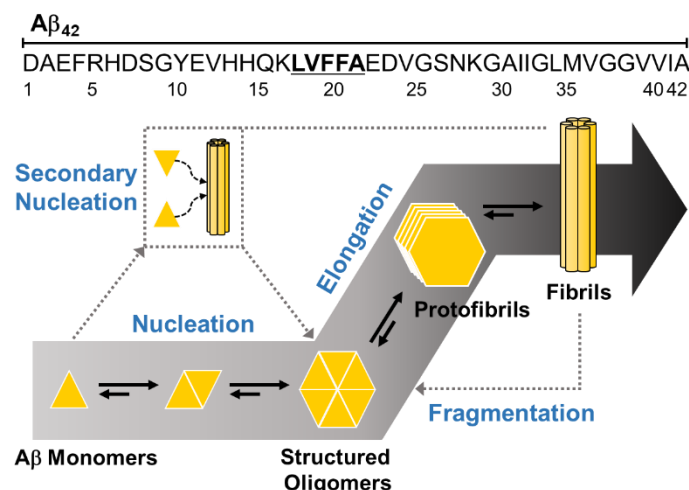


Figure 1.2. Schematic representation of the on-pathway aggregation of A β . During the nucleation phase, A β monomers aggregate to oligomers through interactions between their self-recognition sites (LVFFA; highlighted in bold and underlined in the amino acid sequence of A β). Structured A β oligomers are implicated as potential toxic species. Oligomeric A β species are further transformed into protofibrils and fibrils. Fragmentation of preformed fibrils, along with secondary nucleation, also contributes to the formation of A β oligomers.

NFTs, the second prominent histopathological feature of AD, are mainly found within neurons and predominantly contain aggregates of the tau protein.^{123,144} Proponents of the tau hypothesis links the toxicity in AD to the pathogenicity of tau, whose NFT burden correlates more accurately with neurodegeneration than A β plaque load.^{37,60} Tau, a phosphoprotein, belongs to the family of microtubule-associated proteins (MAPs) that stabilize microtubules, promote, among other functions, anterograde (nucleus to periphery) and retrograde (periphery to nucleus) axonal transport, and sustain dendrite structure.⁶¹ Thus, properly functioning tau is essential to neuronal trafficking and synapse architecture.

Tau is encoded by a single gene on chromosome 17 that gives rise to six isoforms varying in length from 352 to 441 amino acids, which are all found aggregated and hyperphosphorylated in NFTs.^{37,58} Tau hyperphosphorylation causes a loss-of-function, which hinders its ability to bind to microtubules, inducing the deterioration of axonal trafficking and dendrite structure leading to microtubule depolymerization.^{37,58,62} pTau aggregation occurs in stages, as for A β , first into oligomers and amorphous tangles that mature into paired helical filaments (PHFs) and straight filaments (SFs). Similar to A β fibrils, PHFs and SFs also contain a cross- β structural feature but additionally include a β -helix motif.⁶³ Other proteins [e.g., normal tau and alternative MAPs (MAP1/2)] and post-translationally modified and truncated tau/ptau are coaggregated with PHFs and SFs.⁶⁴ A greater understanding of tau's aggregation pathway may prove useful in the development of tau-targeting therapeutics. Noble et al. linked the initiation of tau aggregation to cyclin-dependent kinase-5 (cdk5) in

a transgenic (Tg) mouse model.⁶⁵ Further research regarding tau phosphorylation and aggregation in AD is necessary to determine their cause-and-effect relationship leading to neuronal degradation and suggest prospective therapeutic approaches.

Gain-of-toxic function from tau is suspected to arise from ptau oligomers rather than from NFTs or SFs. Recent studies on the tau oligomers have increasingly supported their role in the early pathology of AD since they could disrupt anterograde axonal transport and impair long-term potentiation (LTP) in Tg mice.^{66,67} For the above-mentioned reasons, the modulation of abnormal hyperphosphorylation and aggregation of tau presents a potential approach for drug discovery. Aside from AD, the diseases, known as tauopathies [e.g., sporadic corticobasal degeneration, progressive supranuclear palsy, and frontotemporal dementia (FTD)], have been linked to tau, suggesting a mutual connection among multiple neurodegenerative diseases.⁶⁸

Increasing evidence indicates a link between the amyloidogenic proteopathy and tauopathy in AD.⁶⁹ Tau and ptau have been reported to directly and indirectly interact with A β . In a perspective article introducing the amyloid cascade hypothesis, A β was accountable for the formation of NFTs.³⁶ The parallel between A β and tau with respect to the toxicity of oligomeric forms has led to the suggestion that the oligomeric species of A β and tau may synergistically act to induce neurotoxicity and synaptic dysfunction.^{69–72} Moreover, the disruption of calcium homeostasis, glycogen synthase kinase 3 (GSK3), cdk5, and free fatty acids have been implicated as bridging factors between A β and tau.^{36,62,65,73,74} The interrelationship of A β and tau appears to be complex, and further clarification would benefit from agents capable of interacting with both of them.

1.2.2. Metal Ions

Metal ions are involved in biologically vital processes, such as signal transmission, catalysis, stabilization of proteins' structures, and metabolism.^{10,75} The functions of the essential first-row transition metals (e.g., Fe, Cu, and Zn) have been widely studied. These metal ions are strongly regulated across the BBB due to their pertinent role in biologically essential processes.⁷⁶ Therefore, the dysregulation of these regulatory mechanisms could lead to disease. In fact, previous studies have demonstrated the colocalization of the above-mentioned metal ions in SPs from AD patients' brain tissue.^{8,10} The metal ion hypothesis posits that the dyshomeostasis and miscompartmentalization of metal ions contribute to AD pathology.⁷⁷ In this section, we discuss metals' functionality, toxicity, homeostasis, and binding to A β , as well as the pathological implications of metal–A β .

Among essential transition metals, Zn is the second-most abundant in biological systems.⁷⁸ Available in both protein-bound and labile forms in the body, Zn(II) is a d¹⁰ metal ion that does not possess a biologically relevant redox activity.⁷⁸ Zn(II) sites in proteins are tetrahedral or distorted tetrahedral, and as a transition metal ion with borderline hardness, Zn(II) binds to nitrogen (N), oxygen

(O), and sulfur (S) donor atoms of amino acid residues.^{79,80} Zn(II) is heterogeneously distributed throughout the brain with relatively high concentrations observed in the hippocampus, amygdala, neocortex, and olfactory bulb areas.⁸¹ Protein-bound Zn(II) [e.g., zinc finger proteins and Cu/Zn superoxide dismutase1 (SOD1)] accounts for over 90% of the total Zn(II) content of the brain. The remaining labile pools of Zn(II), primarily localized within synaptic vesicles of glutaminergic neurons, have been indicated in LTP.^{78,82} The interactions of Zn(II) with γ -aminobutyric acid (GABA) receptors and NMDARs and its extracellular release following neuronal stimulation have led researchers to propose its involvement as a neurotransmitter and secondary messenger.^{83–85}

Cu, the third-most abundant transition metal in the human body, is found in protein-bound [e.g., cytochrome c oxidase (CcO), Cu/Zn SOD1, ceruloplasmin, and dopamine β monooxygenase (D β M)] and labile forms.^{78,86} As a redoxactive metal, Cu acts as a critical cofactor involved in enzymatic functions, including the biochemistry of dioxygen (O₂).^{78,87} The two major oxidation states of Cu are +1 and +2. Cu(I) exists under intracellular reducing conditions, while Cu(II) is likely to be present under oxidizing conditions. Cu(I) and Cu(II) are considered soft and borderline acids, respectively, and bind to N, O, and S donor atoms. Cu(I), like Zn(II), is a d¹⁰ metal ion with preferred coordination numbers 2, 3, or 4, indicating linear, trigonal planar, or (distorted) tetrahedral geometries, respectively. As a d⁹ metal ion, Cu(II) can be coordinated to 4, 5, or 6 ligands, with square planar, square pyramidal, or (axially distorted) octahedral geometries, respectively.⁸⁸

Cu(I)/Cu(II)-coordinated proteins can be categorized into two groups based on their relation to metal ions: (i) proteins utilizing the redox chemistry of Cu(I)/Cu(II) to carry out specific functions (e.g., SOD1 and CcO) and (ii) proteins involved in the Cu transport [e.g., CTR1, ATP7, and CCS].^{9,89} Cu adopts important roles in the brain. In order to compensate for the high level of O₂ metabolism in the brain and the potential accidental release of ROS, neurons and glia require Cu for antioxidant enzymes (e.g., SOD1). Cu is also associated with the homeostasis of neurotransmitters, neuropeptides, and dietary amines by acting as a cofactor for D β M, peptidylglycine α -hydroxylating monooxygenase, tyrosinase, and amine oxidases.⁷⁸ Micromolar Cu is released into the extracellular space upon neuronal depolarization.⁹⁰ Although the role of Cu in signal transmission is not fully understood, previous reports suggest that micromolar Cu is capable of antagonizing NMDA, GABA, and glycine receptors.⁹¹ In addition, exogenous Cu is reported to affect K(I) and Ca(II) channels.⁷⁸ Further research regarding the link of labile Cu(II) to neurotransmission is necessary to gain a better understanding of its neurophysiological role.

Fe, known for its role in O₂ transport and metabolism, is the most abundant transition metal in the human body.^{92,93} Like Cu, the utility of Fe as a redox-active component manifests the basis of its enzymatic involvement. Fe is an essential element of enzymes (e.g., heme proteins, nonheme proteins, and Fe SOD1) responsible for a spectrum of biological functions, such as electron transfer, O₂ chemistry, gene regulation, and regulation of cell growth and differentiation.⁹⁴ The resting state of Fe in enzymes

is mainly found as Fe(II) and Fe(III), while higher oxidation states can be observed as intermediates in catalytic cycles.⁷⁸ Labile Fe(II) and Fe(III) are reported to exist in pools at intracellular concentrations of up to 100 μM ,⁷⁸ but the nonenzymatic role of Fe in neurobiology has not been clearly identified.

Metal ion homeostasis, balancing functionality against toxicity, is a critical aspect in the proper functioning of biological systems.^{78,95} Zn(II) homeostasis is managed by proteins, such as SLC30A (zinc transporter 3; ZnT-3), Zinc-regulated transporters, iron-regulated transporter-like proteins (ZIPs), and metallothioneins (MTs).^{78,96–98} ZIP transporters bring Zn(II) into the cytoplasm, while zinc transporter (ZnT), voltage-gated calcium channels, and NMDARs are shown to mediate the extracellular release of Zn(II).⁹ Greenough and co-workers implicated the expression of presenilins, a component of γ -secretase, as a major contributor toward the control of Zn(II) and Cu(I)/Cu(II) in the brain.⁹⁹ The dysregulation of Zn(II) can lead to excitotoxicity that may induce cell death via the upregulated activity of glutamate receptors, ROS generation, and overactivation of nitric oxide (NO) signaling.^{98,100,101} Cu(I)/Cu(II) homeostasis is regulated by proteins, such as CCS, CTR1, ATP7A, COX17, and Cu metabolism COMM domain-containing protein 1 (COMMD1) domain.^{9,89} On the basis of its redox activity, the dysregulation of Cu(I) and Cu(II) can cause the overproduction of ROS leading to oxidative stress. In addition, due to its imperative roles in enzymes, such as SOD1, CcO, and D β M, the colocalization of Cu in amyloid plaques may result in Cu-deficient proteins, causing irregularity in biological functions. Similar to Cu, the notable redox reactivity of Fe makes it a double-edged sword, enabling a wide range of biological functions but generating ROS, whose release can induce toxicity if unregulated and left unchecked. Fe homeostasis is controlled by different types of proteins, including Fe transporters [e.g., divalent metal-ion transporter-1 (DMT1), ferroportin-1, mitoferrin-1, and ZIP14],¹⁰² heme transporters (e.g., HRG1 and FLVCR1),^{103,104} Fe chaperones (e.g., PCBP), ferrireductases, hepcidin, ferritin, and transferrin.¹⁰⁵

The essential function of metals in the brain coupled with the detrimental effects of their dysregulation suggests that metal ion dyshomeostasis could lead to disease.^{8,9,10,86,106–111} In 1994, Bush et al. discovered the relevance of metal ions in AD pathogenesis.¹¹² They reported the induction of A β_{40} fibrillization in the presence of Zn(II),¹¹² launching intense research into the binding of transition metal ions to A β .¹⁵ Moreover, highly concentrated Cu(I/II), Zn(II), and Fe(II/III) (ca. 400, 1000, and 900 μM , respectively) were found within SPs compared to healthy age-matched controls, reinforcing their interaction with A β in vivo and possible involvement in AD pathogenesis.¹¹³ Since binding of Zn(II), Cu(I/II), and Fe(II) to A β modifies its aggregation, the investigations of molecular-level interactions between metal ions and A β can be challenging. Researchers circumvented this issue by employing A β_{16} or A β_{28} that bind Cu(II) and Zn(II) without significant aggregation.^{114–131} The proposed coordination of Zn(II), Cu(I/II), and Fe(II) to A β is summarized in Table 1.2 and Figure 1.3.

Table 1.2. Proposed amino acid residues of A β for metal coordination.

Metal Ions	Peptides	Amino Acid Residues for Metal Coordination	Technique	Reference
Fe(II)	A β ₁₆ and A β ₄₀	N-terminal NH ₂ , (D1 or E3), (D1-A2 or H6-D7; Carbonyl from the Amide Group), H6, and (H13 or H14)	NMR	129
Fe(III)	A β ₂₈	n.d. ^a	NMR, ESI-MS	130
Cu(I)	A β ₆₋₁₄	H13 and H14	EXAFS	123
	A β ₁₀₋₁₄	H13 and H14	EXAFS	123
	A β ₁₆	H13 and H14	EXAFS, EPR	124
	A β ₁₆	H13 and H14	NMR, XANES	125
	A β ₁₆	H13 and H14	CP-MD Simulation	126
	A β ₄₀	H13 and H14	EXAFS, EPR	124
Cu(II)	A β ₁₆	pH 6.5: H6, (H13 or 14), N-terminal NH ₂ , (D1; Side-chain Carboxylate Group), and (D1-A2; Carbonyl from the Amide Group)	EPR	134
		pH 9.0: N-terminal NH ₂ , (D1-A2; N from the Amide Group), (A2-E3; Carbonyl from the Amide Group), and (H6, H13, and H14)		
	A β ₁₆	pH 6.3: N-terminal NH ₂ , (D1-A2; Carbonyl from the Amide Group), H6, and (H13 or H14); pH 8.0: (A2-E3; Carbonyl from the Amide Group), H6, H13, and H14	EPR	127
	A β ₁₆	pH 6.3: D1, (D1-A2; Carbonyl from the Amide Group), H6, and (H13 or H14); pH 8.0: (A2-E3; Carbonyl from the Amide Group), H6, H13, and H14	EPR	128
	A β ₂₈	pH 5.5: H6, Y10, H13, and H14	NMR, EPR	119
	A β ₂₈	pH 7.4: N-terminal NH ₂ , H6, H13, and H14	EPR	138
Zn(II)	A β ₁₆	R5, H6, H13, and H14	ESI-MS	114
	A β ₁₆	D1, H6, H13, and H14	NMR	115

A β ₁₆	H6, H13, H14, and (E11; Side-chain Carboxylate Group)	NMR	116
A β ₁₆	A β ₁₁₋₁₄ Residues (E11 and H14)	SPR, ESI-MS	117
pA β ₁₆ (S8)	H6, D7, Phosphorylated S8, E11, H13, and H14	ITC, ESI-MS, NMR	118
N-terminal acetylated A β ₁₆	H6, E11, (H13 or H14), (D1, E3, or D7), and N-terminal NH ₂	NMR, XAS	131
D7H-A β ₁₀	(D1-A2; Carbonyl from the Amide Group), E3, H6, and H7	NMR, EXAFS, MS, ITC	122
A β ₂₈	H6, H13, and H14	NMR, EPR	119
A β ₂₈	H6, H13, and H14	NMR, CD	120
A β ₂₈	N-terminal NH ₂ , H6, H13, (H14, and/or E11), and (Y10 for Conformational Rearrangement)	NMR	121
A β ₄₀	N-terminal NH ₂ , H6, H13, and H14	NMR	132

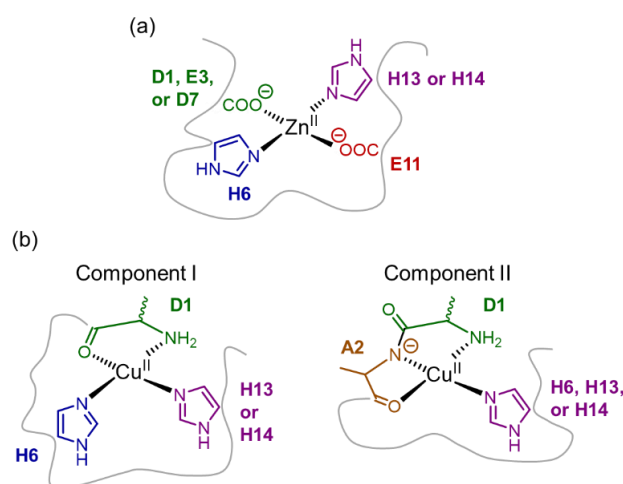


Figure 1.3. Examples of metal coordination to A β . Each metal [Zn(II) and Cu(II)] coordination is published in refs 131 and 134, respectively. Possible fifth ligands on the metal centers are not indicated in this figure.

Numerous studies have focused on possible binding modes of Zn(II) and A β .^{114–122,131,132} On the basis of previous findings, the feasible Zn(II) binding sites in A β are primarily composed of 4–6 ligands: H6, H13, and/or H14 with additional candidates that include D1 (N-terminal NH₂ or side chain carboxylate), E3, R5 (backbone amide), D7, Y10, E11, or water molecules.^{8,106,108,114–116,119,120,132,133} In

addition, Y10 is implicated in a Zn(II)-dependent conformational rearrangement under membrane-mimicking environments.¹²¹ Kulikova et al. reported that phosphorylated residues may be involved in Zn(II) binding based on studies with A β containing phosphorylated S8 (pA β). Proposed binding residues are the phosphate group, the imidazole ring of H6, and a backbone carbonyl group of either H6 or D7.¹¹⁸ This binding mode stimulates peptide dimerization with an additional Zn(II) coordinated to two pairs of E11 and H14 from two separate peptide subunits.¹¹⁸ This observation of Zn(II)-induced dimerization provides insight into the initiation of metal-induced A β aggregation.

Recently, an unprecedented coordination of Zn(II)-A β ₁₀ was presented with the Taiwanese mutation D7H using a suite of structural characterization methods.¹²² The 1:1 stoichiometry was confirmed via nuclear magnetic resonance (NMR) and isothermal titration calorimetry (ITC). Additionally, the formation of the proposed complex [Zn₂(D7H-A β ₁₀)₂], which consisted of a binuclear Zn(II) core where both ions were bound to two D7H-A β ₁₀ peptides, was validated by mass spectrometry (MS) and isotope-edited NMR.¹²² The NMR investigations revealed that the carbonyl group (D1-A2), carboxyl group (E3), H6 (from one polypeptide chain), and H7 (from the second polypeptide) were bound to Zn(II).¹²² These observations were theoretically refined and supported by extended X-ray absorption fine structure (EXAFS) spectroscopy.¹²²

The Cu(II)-A β binding mode occurs in two forms, components I and II (Figure 1.3), depending on the pH (i.e., pH 6.5 and pH \geq 8, respectively).^{8,106,119,127,128,133-137} At pH \geq 8, component II is predominant with three main potential binding configurations of Cu(II)-A β : (i) 3N1O coordination {e.g., for 3N, [H6, D1 (N-terminal NH₂), and D1-A2 (deprotonated backbone amide)] or (H6, H13, and H14); for 1O, carbonyl backbone oxygen (A2-E3)},^{127,128,134} (ii) 4N coordination with three histidines (H6, H13, and H14) and either N-terminal amino group or deprotonated backbone amide,^{138,139} or (iii) 5N1O coordination with potential binding sites: N-terminal NH₂, the N donor atom from the D1-A2 backbone, carbonyl backbone from A2-E3, H6, H13, and H14.¹³⁴

Component I is the prevalent Cu(II) binding mode with A β under physiological conditions. Several reports have proposed 3N1O coordination involving: (i) the N-terminal primary amino group of D1, an O donor atom from a carbonyl backbone between D1 and A2, H6, and either H13 or H14 or (ii) D1 (N-terminal amine), D1-A2 (a carbonyl backbone), and two histidines among H6, H13, and H14, with the possibility of an additional coordination with D1 (carboxylate).^{8,106,108,127,128,133-136} Dorlet et al. reported the observation of a 5-coordination mode using electron paramagnetic resonance spectroscopy (EPR) in conjunction with specific isotopic labeling.¹³⁴ They detected and identified a 3N2O coordination site in A β consisted of two histidines (H6 and either H13 or H14), the N-terminal NH₂, the carbonyl group between D1 and A2, and the carboxylate group of D1. The carbonyl and carboxylate groups from D1 were reported in the equatorial and axial positions, respectively. The exact binding atoms of D1 in A β is controversial. The N-terminal NH₂, the carboxylate, and the amide backbone have

all been suggested to be possible binding atoms from D1.^{127,128,134} Moreover, the involvement of Y10 via conformational rearrangement of Cu(II)–A β at pH 6.9 has been suggested.¹¹⁹ Previous studies demonstrated that the pH-dependent oxidation state of the A β -bound Cu dictates the coordination geometry of the complex.^{124,140} When Cu K-edge X-ray absorption spectroscopy (XAS) was applied to Cu(II)–A β , a square-planar Cu(II) center with mixed N/O ligation, including imidazole groups of histidine ligands, was indicated.^{124,141} After reduction of Cu(II)–A β , the EXAFS data fit best a linear two-coordinate geometry with two imidazole ligands, possibly H13 and H14, coordinated to Cu(I)–A β .^{123–126,141} Studies of the Fe(II)–A β binding via NMR demonstrated a coordination composed of the N-terminal NH₂ (D1), a carboxylate from either D1 or E3, a carbonyl group from D1-A2 or H6-D7, and two N donor atoms from H6 and either H13 or H14.¹²⁹ There is limited information regarding the binding of Fe(III)–A β .^{129,130}

Determination of binding affinities of metal–A β complexes at different conditions can be valuable, especially towards the development of therapeutics with metal chelating capabilities. Comparative studies regarding binding affinities of metal–A β to novel metal chelators may allow researchers to estimate their ability to target labile metal ions and metal–A β versus metal ions from metalloproteins essential for biological functions. The reported range of K_d for Zn(II) and A β is 10^{-9} – 10^{-6} M.^{8,108,132,135,142–148} The presented K_d values for metal–A β are dependent on the experimental conditions and techniques, such as ITC, fluorescence spectroscopy, and potentiometry.^{108,110,132,143–146} For Cu(II)–A β , the K_d value was calculated to be 10^{-11} – 10^{-7} M, while Cu(I)–A β showed 10^{-15} – 10^{-8} M in K_d .^{8,107,132,135,138,142,144–146,149–160} Cu(II) seems to exhibit stronger binding to A β than Zn(II). Fe(II) forms less stable complexes (K_d = ca. 10^{-5} M), compared to those of Cu(II) or Zn(II).¹⁴⁵ The reported K_d values of Zn(II)–A β , Cu(I/II)–A β , and Fe(II)–A β are summarized in Table 1.3. The propensity of A β to aggregate poses a challenge in studying its metal binding properties. As a solution, researchers have been utilizing various A β fragments with slower aggregation kinetics. Although soluble A β fragments enable the study of metal binding and coordination, various conformations of the full-length A β (e.g., monomers, oligomers, and fibrils) are expected to exhibit different metal coordination environments.^{146,159} On the basis of currently available literature, a wide range of binding affinities is reported because metal binding to A β is dependent on A β species, techniques, and experimental conditions (e.g., buffer composition, temperature, concentrations, and peptide purity).

Table 1.3. Binding affinities of metal ions to A β .

Metal Ions	Peptides	K_d ($\times 10^{-6}$ M)	Conditions ^a	Technique	Reference
Fe(II)	A β_{40}	76 (\pm 20)	10 mM Tris, pH 7.4, 100 mM NaCl	Fluorescence	145
	A β_{16}	2.7 (\pm 2.1) $\times 10^{-9}$	20 mM <i>N</i> -Ethylmorpholine, pH 7.0	UV-Vis	154
	H6A-A β_{16}	8.9 (\pm 3.7) $\times 10^{-9}$	20 mM <i>N</i> -Ethylmorpholine, pH 7.0	UV-Vis	154
Cu(I)	H13A-A β_{16}	1.1 (\pm 0.7) $\times 10^{-8}$	20 mM <i>N</i> -Ethylmorpholine, pH 7.0	UV-Vis	154
	H14A-A β_{16}	1.0 (\pm 0.8) $\times 10^{-8}$	20 mM <i>N</i> -Ethylmorpholine, pH 7.0	UV-Vis	154
	A β_{42}	5.4 (\pm 0.9) $\times 10^{-2}$	100 mM HEPES, pH 7.4	UV-Vis	154
Cu(II)	A β_{16}	47 (\pm 5)	100 mM Tris, pH 7.4, 150 mM NaCl	Fluorescence	149
	A β_{16}	0.1	H ₂ O, pH 7.8	Fluorescence	150
	A β_{16}	0.09	50 mM HEPES, pH 7.4, 100 mM NaCl	ITC	151
	A β_{16}	0.7 $\times 10^{-3}$	20 mM HEPES, pH 7.2, 150 mM NaCl	ITC	158
	A β_{16}	0.3 $\times 10^{-3}$	20 mM PIPES, pH 7.4, 160 mM NaCl	ITC	160
	A β_{4-16}	8 (\pm 2)	100 mM Tris, pH 7.4, 150 mM NaCl	Fluorescence	149
	A β_{28}	0.1	H ₂ O, pH 7.8	Fluorescence	138
	A β_{28}	28 (\pm 5)	100 mM Tris, pH 7.4, 150 mM NaCl	Fluorescence	149
	A β_{28}	0.07	50 mM HEPES, pH 7.4, 100 mM NaCl	ITC	151
	A β_{28}	0.4 (\pm 0.1)	10 mM Phosphate, pH 7.2	Fluorescence	156
	A β_{28}	2.5 (\pm 0.2)	10 mM HEPES, pH 7.2	Fluorescence	156
	A β_{28}	1.2 (\pm 0.1)	10 mM Phosphate, pH 6.5	Fluorescence	156

	A β ₄₀	1.6 (\pm 0.9)	10 mM Tris, pH 7.4, 100 mM NaCl	Fluorescence	145
	A β ₄₀	11 (\pm 1)	100 mM Tris, pH 7.4, 150 mM NaCl	Fluorescence	149
	A β ₄₀	ca. 8	50 mM Phosphate, pH 7.4, 100 mM NaCl	Fluorescence	152
	A β ₄₀	0.5 (\pm 0.2)	10 mM Tris, pH 7.4, 100 mM NaCl	Fluorescence	144
	A β ₄₀	1.2 (\pm 0.4)	20 mM Tris, pH 7.4, 100 mM NaCl	Fluorescence	144
	A β ₄₀	3.8 (\pm 0.9)	50 mM Tris, pH 7.4, 100 mM NaCl	Fluorescence	144
	A β ₄₀	30 (\pm 6)	100 mM Tris, pH 7.4, 100 mM NaCl	Fluorescence	144
	A β ₄₀	0.6 (\pm 0.2)	20 mM HEPES, pH 7.4, 100 mM NaCl	Fluorescence	144
	A β ₄₀	2.5 (\pm 0.6)	100 mM HEPES, pH 7.4, 100 mM NaCl	Fluorescence	144
	A β ₄₀	0.9 x 10 ⁻³	20 mM HEPES, pH 7.2, 160 mM NaCl	ITC	155
	A β ₄₀	0.4 x 10 ⁻³	20 mM HEPES, pH 7.4, 160 mM NaCl	ITC	155
	A β ₄₀	1.6	5 mM Phosphate, pH 7.3	NMR	157
	A β ₄₀	5.2 x 10 ⁻⁴	20 mM PIPES, pH 7.4, 160 mM NaCl	ITC	160
	F4W-A β ₄₀	0.6 (\pm 0.2)	10 mM Tris, pH 7.4, 100 mM NaCl	Fluorescence	155
	A β ₄₂	2.0 (\pm 0.8)	10 mM Tris, pH 7.4, 100 mM NaCl	Fluorescence	155
	A β ₄₂	0.8 (\pm 1.0)	20 mM HEPES, pH 7.4, 100 mM NaCl	Fluorescence	154
Zn(II)	A β ₁₆	22 (\pm 15)	20 mM Tris, pH 7.4, 100 mM NaCl	ITC	153
	A β ₁₆	14 (\pm 5)	20 mM HEPES, pH 7.4, 100 mM NaCl	UV-Vis	153
	A β ₁₆	9	50 mM HEPES, pH 7.1	UV-Vis	148

A β ₂₈	6.6 (\pm 0.2)	10 mM HEPES, pH 7.2	Fluorescence	132
A β ₂₈	1.1 (\pm 0.1)	10 mM Phosphate, pH 7.2	Fluorescence	132
A β ₂₈	3.2 (\pm 0.1)	10 mM Phosphate, pH 6.5	Fluorescence	132
A β ₂₈	12 (\pm 5)	20 mM HEPES, pH 7.4, 100 mM NaCl	UV-Vis	143
A β ₂₈	10 (\pm 8)	20 mM Tris, pH 7.4, 100 mM NaCl	ITC	143
A β ₄₀	1.2 (\pm 0.03)	10 mM Phosphate, pH 7.2	NMR	132
A β ₄₀	300 (\pm 100)	10 mM Tris, pH 7.4, 100 mM NaCl	Fluorescence	145
A β ₄₀	7 (\pm 3)	20 mM Tris, pH 7.4, 100 mM NaCl	ITC	143
A β ₄₀	7 (\pm 3)	20 mM HEPES, pH 7.4, 100 mM NaCl	UV-Vis	143
A β ₄₀	65 (\pm 3)	20 mM HEPES, pH 7.4, 100 mM NaCl	Fluorescence	144
A β ₄₀	124 (\pm 32)	20 mM HEPES, pH 7.4, 100 mM NaCl	UV-Vis	144
A β ₄₀	60 (\pm 14)	10 mM Tris, pH 7.4, 100 mM NaCl	Fluorescence	144
A β ₄₀	184 (\pm 30)	100 mM Tris, pH 7.4, 100 mM NaCl	Fluorescence	144
A β ₄₀ fibrils	9 (\pm 6)	20 mM HEPES, pH 7.4, 100 mM NaCl	UV-Vis	143
F4W-A β ₄₀	90 (\pm 30)	10 mM Tris, pH 7.4, 100 mM NaCl	Fluorescence	145
A β ₄₂	57 (\pm 28)	10 mM Tris, pH 7.4, 100 mM NaCl	Fluorescence	145
A β ₄₂	7 (\pm 3)	20 mM HEPES, pH 7.4, 100 mM NaCl	UV-Vis	143
A β ₄₂	91 (\pm 16)	20 mM HEPES, pH 7.4, 100 mM NaCl	Fluorescence	144
A β ₄₂	6.2 (\pm 0.9)	20 mM HEPES, pH 7.4	ITC	147

^aTris, tris(hydroxymethyl)aminomethane; HEPES, 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid; PIPES, piperazine-*N,N'*-bis(2-ethanesulfonic acid); PBS, phosphate-buffered saline.

The influence of transition metal ions on A β aggregation has also been examined in depth since the first description of Zn(II)-dependent A β ₄₀ aggregation.^{11,112,161} At physiological pH, Cu(II) and Fe(II/III) also promote A β ₄₀ aggregation,^{161,162} although induction by Cu(II) requires a slightly acidic condition (e.g., pH 6.8).¹⁶³ Even trace metal ions (< 0.8 μ M) are sufficient to stimulate A β ₄₀ aggregation, resulting in less structured aggregates.^{164,165} Metal-induced A β aggregation is shown to be rapid, and it could result in the production of nonfibrillar, amorphous aggregates depending on the ratio of metal to A β (vide infra). A mixture of A β ₄₂:Cu(II) in a 1:5 ratio resulted in a diminished fluorescence intensity of thioflavin-T (ThT), and smaller-sized aggregates as determined by atomic force microscopy (AFM), relative to A β ₄₂ only.¹⁶⁶ This observation was extended to other metal ions, including Zn(II) and Fe(II).¹⁶⁷ Ultrafast spectroscopic techniques demonstrated an immediate interaction within milliseconds between micromolar Zn(II) and A β ₄₀ showing resultant nonfibrillar peptide aggregates that were possibly toxic.¹⁶⁸ A detailed study suggested that Zn(II)-A β ₄₀ species might inhibit fibril formation by disrupting fibril elongation.¹⁶⁹ Interaction of Cu(II) with A β ₄₀ (pH 6.7) was also observed on a time scale of subseconds with the formation of amorphous Cu(II)-A β species.¹⁷⁰ Likewise, Fe(III) was observed to retard A β ₄₂ fibrillization by redirecting the aggregation pathways towards unstructured, less toxic Fe(III)-A β aggregates.¹⁷¹ Although the precise nature of metal-A β conformations is uncertain, the measurements by circular dichroism spectroscopy (CD) propose that their transition may involve the generation of β -enriched structures, distinct from the fibrillar β -sheet conformation.¹⁷²

Metal ions appear to increase the proportion of soluble oligomers compared to fibrils.¹⁷³⁻¹⁷⁵ Since structured soluble oligomers are associated with toxicity,^{176,177} this may constitute a potential mechanism of toxicity that arises from metal-A β species. Addition of Cu(II) to A β yielded soluble toxic oligomers enriched in a β -sheet configuration.¹⁷⁴ In another report, Cu(II) and Zn(II) triggered the production of transient A β oligomers.¹⁷⁵ While Zn(II) developed annular A β protofibrils without undergoing a nucleation process, Cu(II) and Fe(III) prevented the formation of fibrils by lengthening the nucleation phase.¹⁷⁵

The relative ratio of metal ions to A β also impacts the aggregation pathways of A β .^{178,179} Increasing the relative amount of Cu(II) to A β ₄₀ from 0.1 to 0.6 causes a shift from fibrillar structures to amorphous granular aggregates.¹⁷⁸ Another study examined a wider Cu(II):A β ₄₀ range from sub- to supra-stoichiometric amounts.¹⁷⁹ The Cu(II):A β ratio was found to affect the aggregation kinetics and aggregate morphology, deviating from fibrillar to nonfibrillar with increasing Cu(II):A β proportions. Structures of Cu(II)-A β aggregates were dynamic. The transient and impermanent nature of metal-A β species has made their structural characterization difficult. Still, progress towards an understanding of their general characteristics has been made. A small-angle X-ray scattering (SAXS) study examined the generation of A β oligomers at extremely short time scales by combining the technique with in-line rapid

mixing.¹⁸⁰ Modeling of the scattering data can approximate oligomers' size (i.e., diameter), molecular weight, and polydispersity.

Although the aggregation kinetics, species distribution, and toxicity of metal-A β species have been extensively studied, their precise mechanism of toxicity has been still uncertain. Recently, Matheou et al. illustrated the distinct influence of substoichiometric Cu(II) on the aggregation pathways of A β ₄₀ and A β ₄₂.¹⁸¹ While fibrillization was favored for A β ₄₀, oligomeric and protofibrillar forms of A β ₄₂ were observed in the presence of Cu(II). These species could cause leakage from lipid vesicles in a manner reminiscent of metal-free A β oligomers.¹⁸² Mutations of A β may also impact its aggregation properties in the presence of metal ions and may be one mechanism linking familial forms of AD to pathogenesis. The Taiwanese mutation (D7H) led Zn(II)- and Cu(II)-induced aggregates of both A β ₄₀ and A β ₄₂ from fibrillar forms to smaller-sized oligomers.¹⁸³ The pathogenic A2V mutation imparted different A β aggregation kinetics and metal binding properties in response to addition of Cu(II).¹⁸⁴ The Cu(II)-A β ^{A2V} complex showed a preference for the component I configuration of the Cu(II) center.

On the basis of cumulative experimental and theoretical evidence, metal ions have been considered potential therapeutic targets in AD. The utilization of metal chelators has demonstrated their potential as AD treatments, but further optimization of metal chelators is necessary to develop effective therapeutics.^{185,186} Moreover, fine-tuning metal binding affinities (K_d) of compounds to specifically target metal ions bound to A β without disrupting vital enzymatic activities is an important parameter for rational design.

1.2.3. Oxidative Stress

O₂ is indispensable to aerobic organisms. In metabolic systems, ROS are generated from endogenous processes, such as O₂ metabolism and cellular signaling, while exogenous ROS can be produced from environmental stress (e.g., ionizing radiation and heat exposure).^{187–189} Biologically relevant ROS include superoxide anion radical (O₂^{•−}), hydroxyl radical (•OH), hydrogen peroxide (H₂O₂), hydroperoxyl radical (•O₂H), singlet oxygen (¹O₂), peroxide (O₂^{2−}), and hydroxide ion (OH[−]). A membrane-bound enzyme, nicotinamide adenine dinucleotide phosphate oxidase (NADPH oxidase), found in cell membranes, mitochondria, and ER, is responsible for substantial intracellular ROS production.^{190,191} NADPH oxidase generates superoxide anion radicals (O₂^{•−}) by transferring electrons from NADPH within the cell across the membrane.^{190,192} ROS are necessary for a variety of cellular functions, including receptor-mediated signaling pathways and transcriptional activation.^{193–199} In addition, ROS plays a critical role in cellular homeostasis through regulation of apoptosis. ROS control apoptotic signaling initiated via two pathways:^{198,200} (i) ROS-triggered death receptors [e.g., Fas (CD95 or APO-1), tumor necrosis factor (TNF) receptor 1, TNF-related apoptosis-inducing ligand (TRAIL) receptor 1 (TRAIL-R1 or DR4), and TRAIL receptor 2 (TRAIL-R2 or DR5)] can mediate the extrinsic

pathway of apoptosis by clustering and forming lipid-raft-derived signaling platforms, suggested as a major mechanism of apoptotic signaling,^{200,201} and (ii) ROS are associated with mitochondrial permeabilization by generating pores in the mitochondrial outer membrane, which stimulates the release of proapoptotic proteins [e.g., members of the B-cell lymphoma 2 (Bcl-2) gene family and BAX (Bcl-2 associated X)] that are essential for the activation of apoptosis.^{198,200,202–204}

Various types of ROS can be found in cellular environments.^{193,194} Prominent biological ROS are hydroxyl radical ($\bullet\text{OH}$), $\text{O}_2^{\bullet-}$, and H_2O_2 . Hydroxyl radicals are produced by Fenton-like reactions.^{8,142} Due to its relatively short half-life (10^{-9} s), $\bullet\text{OH}$ is known to be involved in “site-specific” reactions in the vicinity of its formation site.^{205,206} $\text{O}_2^{\bullet-}$, the product of the one-electron reduction of O_2 , is generated by multiple systems in organisms of animals and plants (e.g., xanthine oxidase and NADPH oxidase).^{188,192,194,207} $\text{O}_2^{\bullet-}$ can react with many substrates by converting into other species.^{111,194,195} $\text{O}_2^{\bullet-}$ is capable of transforming into $\bullet\text{OH}$ by the Haber-Weiss reaction, which generates $\bullet\text{OH}$ from H_2O_2 and $\text{O}_2^{\bullet-}$.²⁰⁷ Both $\bullet\text{OH}$ and $\text{O}_2^{\bullet-}$ can initiate lipid peroxidation that can lead to apoptosis.^{8,107,188,195,207,208} H_2O_2 is a common byproduct of diverse enzymatic reactions, including those involving SOD.^{107,111,188,194,195,209} H_2O_2 is related to a broad range of biological processes: (i) immune response; (ii) oxidative biosynthesis, such as tyrosine crosslinking mediated by peroxidases; (iii) cellular signaling in mediating mitogenic signaling pathways.^{195,209,210}

Under normal conditions, the levels of the above-mentioned ROS are regulated by innate antioxidant defenses.^{10,111,190,211–213} Pathological conditions, however, can elicit an imbalance between the production and removal of ROS, resulting in elevated ROS levels.^{9,111,195} Oxidative stress is characterized by dysregulation of ROS and the resultant cellular damage through the oxidation of lipids, proteins, and DNA.^{86,111,189,193–195} Oxidative stress in biological systems has been strongly implicated as a causative factor for a wide spectrum of diseases and aging.^{9,111,195} Thus, maintaining proper ROS load is important to the preservation of biological homeostasis.

Oxidative stress is believed to be involved in neurodegenerative diseases, including AD.^{9,10,86,110,111,142,187–189,208,211,213,214} Oxidative stress is a prevailing component in the manifestation of multiple pathological factors (e.g., $\text{A}\beta$, metal ions, and metal- $\text{A}\beta$) as well as toxic mechanisms of these factors.^{142,107,215} Three major aspects are connected with oxidative stress to AD pathology: (i) $\text{A}\beta$ production and accumulation;^{211,215–218} (ii) metal ion dyshomeostasis;²¹⁹ (iii) mitochondrial dysfunction.^{111,187,189,193,194,214,215} Researchers have suggested that oxidative stress enhances $\text{A}\beta$ production by decreasing the activity of α -secretase while increasing the activity of β - and γ -secretases.^{211,215} In addition, oxidative stress could activate the pathway of c-Jun N-terminal kinase (JNK), which could modulate the expression of β -secretase.^{211,215} The generated $\text{A}\beta$ accumulates in the brain and forms SPs, a hallmark of AD.^{86,109}

Pathological factors of AD (e.g., metal ions, A β , and tau) are suggested to be involved in redox-active processes capable of inducing oxidative stress via ROS generation.^{10,106,220} Multiple *in vitro* and *in vivo* studies report that A β peptides trigger oxidative stress.^{221–236} A *Tg C. elegans* worm model expressing human A β_{42} exhibited enhanced oxidative stress as evidenced by elevated carbonyl levels associated with the oxidation of proteins.^{233,237} I31 and M35 in A β are proposed to be potentially responsible for oxidative damage (*vide infra*).^{228,229,231,237} Especially, M35 is reported as a critical amino acid residue for ROS production.^{221,223,230} The α -helical conformation in the C-terminal region of A β allows the S atom of M35 to interact with the O atom from the carbonyl of I31,^{229,231,236} which could result in the formation of the methionine sulfuranyl radical (MetS \bullet).^{228,236,238} A β can also act as a source of ROS and initiate lipid peroxidation by producing carbon-centered radicals.^{231,236} Moreover, oligomeric A β has been observed to increase the generation of ROS directly by activating NADPH oxidase and indirectly through NMDARs by stimulating the release of arachidonic acid, a retrograde messenger involved in modulating synaptic plasticity.^{232,239}

The dysregulation of redox-active metal ions, including Cu(I/II) and Fe(II/III), in the central nervous system (CNS) is observed in the AD-affected brain.^{240–243} Furthermore, these metal ions are able to produce ROS through Fenton-like reactions.^{244,245} Overproduction of ROS by metal ions can result in oxidative stress that causes neuronal death in the brain.^{10,213,214} Moreover, Zn(II), a redox-inert metal ion, indirectly increases ROS levels.^{246–250} Mitochondrial uptake of labile Zn(II) from the cytoplasm through the calcium uniporter can alter mitochondrial polarization and disrupt the electron transport chain leading to the formation of ROS, such as O $_2^{\bullet-}$.^{246–250}

Along with the individual impact of metal ions and A β on ROS production, metal–A β species have been observed to generate ROS. Redox-active metal ions associated with A β [i.e., Cu(I/II)–A β and Fe(II/III)–A β] can generate ROS via Fenton-like reactions, similar to redox-active metal ions.^{10,251,252} *In vitro* studies demonstrate that Cu(I/II)–A β or Fe(II/III)–A β can overproduce ROS leading to oxidative stress.^{8,10,213,251,253,254} ROS generation mediated by Cu(I/II)–A β has been widely studied.^{86,129,136,255,256} Cu(I/II)–A β is indicated to catalytically form ROS. In the presence of a reductant (e.g., ascorbate), Cu(II)–A β could be reduced to Cu(I)–A β and transfer an electron to O $_2$ to yield O $_2^{\bullet-}$.^{86,255,257} Then, a hydroperoxyl radical (\bullet O $_2$ H) can be formed via electron/proton transfer, finally resulting in the production of H $_2$ O $_2$ (*vide supra*).^{8,10,259} The generated H $_2$ O $_2$ can then react with either Cu(I)–A β or Cu(II)–A β affording \bullet O $_2$ H or \bullet OH through Fenton-like reactions.^{8,86,258} Spectroscopic and spectrometric studies presented that the D1, H13/H14, and M35 residues in A β may be involved in the electron transfer between Cu(I/II) and A β responsible for ROS generation.^{221,230,255,259–263}

Oxidative stress can damage cells by disrupting cell signaling and causing mitochondrial dysfunction.^{111,181,189,193,215} Mitochondrial function is vulnerable to oxidative stress; however, paradoxically, the mitochondrial respiratory chain is a major source of intracellular ROS.^{193,215,264}

Mitochondrial respiratory complexes could generate ROS, such as $O_2^{\bullet-}$ and H_2O_2 , and the increased concentrations of these ROS could produce $\bullet OH$ and react with biomolecules, including lipids and proteins.^{8,188,195,207,265} Biological systems are observed to protect themselves from oxidative stress by maintaining appropriate levels of ROS with endogenous defensive systems.^{107,111,187,193–195} For example, (i) Cu/Zn SOD1 binds to Cu and Zn to catalyze the dismutation of $O_2^{\bullet-}$ into either O_2 and H_2O_2 ;^{9,86,111,188,208} (ii) another important antioxidant is glutathione that is converted to its oxidized form (i.e., glutathione disulfide) upon interaction with ROS;^{188,194} (iii) catalases catalyze the decomposition of H_2O_2 to H_2O and O_2 .^{209,210} Thus, the imbalance between ROS production and removal could occur by deficient antioxidant defense, inhibition of electron flow, or exposure to xenobiotics.²⁶⁵

Oxidative stress is indicated to play an underlying role in the pathology of AD based upon the impact of ROS on the production and aggregation of A β , metal ion homeostasis, and mitochondrial dysfunction. These pathological features could contribute back to oxidative stress through ROS generation in direct and indirect manners. Thus, the utilization of antioxidants to reduce the level of ROS offers a potential approach for drug discovery in AD. The strategy of regulating ROS only with antioxidants, however, has not been successful in clinical trials, possibly due to the multifaceted nature of AD pathology.²⁶⁶

1.2.4. Cholinesterases (ChEs)

The cholinergic hypothesis proposes that the degeneration of cholinergic neurons and the associated loss of cholinergic neurotransmission in the cerebral cortex are contributors to the deterioration of cognitive function observed in the brain of AD patients.^{267,268} ACh, the neurotransmitter in cholinergic transmission responsible for learning and memory in the CNS, is a cationic agonist of muscarinic and nicotinic receptors.^{269,270} ACh production from choline and acetyl coenzyme A (acetyl-CoA) is catalyzed by choline acetyltransferase (ChAT) in neurons.²⁷¹ Cholinergic transmission is initiated by the ACh release from the presynapse into the synaptic cleft, where ACh diffuses and binds to postsynaptic receptors. Subsequently, ChEs, serine hydrolases abundant in the synaptic cleft, rapidly terminate signal transmission by converting ACh into acetate and choline. To complete the cycle of cholinergic transmission, the presynaptic neuronal reuptake of catabolic products occurs to produce ACh. Cholinergic deficits from decreased ACh levels are a characteristic of the brain affected by AD.²⁷² As the main culprit of this phenomenon, ChEs have been widely studied as a therapeutic target for AD leading to the development of AChEIs for AD treatment (Table 1.1). There are two main types of ChEs: (i) AChE and (ii) butyrylcholinesterase (BuChE). AChE is responsible for the majority of the ChE activity in healthy human brains, while the remaining is accounted for by BuChE.^{273,274} AChE has been a therapeutic target in AD based on its role in hydrolyzing the majority of ACh in the brain.^{275,276}

The active site of AChE is located at the bottom of a gorge, a narrow cavity lined with 14 highly conserved aromatic residues.²⁷⁷ The active site of human AChE (hAChE) is composed of an esteratic

site containing the catalytic triad (i.e., S200, H440, and E327), and an anionic site, where the quaternary ammonium of ACh binds through cation- π interactions. Analysis of the crystal structure of AChE revealed that the anionic site, which binds the quaternary trimethylammonium choline moiety of the substrate via cation- π interactions, is in fact uncharged and hydrophobic due to the presence of numerous aromatic residues.^{278–280} The cumulative system of intermolecular interactions and geometric constraints of the active site gorge may contribute to the substrate specificity and rapid enzyme kinetics of AChE through mechanisms, such as aromatic guidance.^{280,281} In addition, the peripheral anionic site (PAS), located near the rim of the gorge, has been reported to transiently bind to substrates as an initiating step of the catalytic process.^{282,283} Szegletes et al. reported that binding of ACh to the PAS of AChE led to accelerated hydrolysis.²⁸³

BuChE can also hydrolyze ACh.^{284,285} BuChE also possesses the overall structure, the amino acid sequence, and the catalytic mechanism similar to AChE.²⁸⁶ While AChE is specific for ACh, BuChE can hydrolyze a range of esters and amides, in addition to ACh. One explanation for this disparity in substrate specificity is the size difference of their active-site gorges. The reported active-site gorge of BuChE (ca. 500 Å) is much larger than that of AChE (ca. 300 Å).²⁸⁷ Furthermore, BuChE lacks the PAS that contributes towards AChE's activity.²⁸⁸ The distinct structural characteristics of the two ChEs present a parameter to consider when compounds capable of inhibiting the activity of either AChE, BuChE, or both are rationally designed.²⁸⁹ The physiological and pathological roles of BuChE remain unclear. Specific inhibitors for AChE and BuChE may help determine their impact on cholinergic transmission and AD pathogenesis. Thus, the potential therapeutic benefits of targeting BuChE, explored less than AChE, could provide a valuable direction for AD research.

In recent years, the lack of success in halting AD progression with ChE inhibitors (ChEIs) has led researchers to reevaluate the cholinergic hypothesis. A comparative study monitoring the levels of cholinergic markers in human subjects with mild cognitive impairment (MCI) and severe late stage of AD suggested that cholinergic dysfunction may be influential during the later stages of the disease.²⁹⁰ Compensatory responses, such as upregulation of ChAT in the frontal cortex and hippocampus, have been proposed as resistance mechanisms working against the transition from MCI to AD.²⁹¹ Based on the current direction in understanding AD pathology, reassessment of the cholinergic hypothesis focuses on the interrelationships between ChEs and other pathological factors, including A β , tau, metal ions, and ROS.^{292–298} Both AChE and BuChE have been found to be colocalized with A β aggregates in SPs.²⁹⁹ Moreover, evidence has indicated that AChEs could affect A β aggregation^{299–302} and toxicity via interactions between the PAS and A β .^{292,299} For example, the complexation of AChE and A β , at the hydrophobic PAS of AChE could accelerate A β aggregation.^{299,301} Further research is needed to fully elucidate the pathological relationships between ChEs and other pathological elements.

1.2.5. Additional Targets

In this section, we briefly introduce additional pathological factors in AD that may serve as therapeutic targets in the design of multifunctional molecules. Glutamate is a central excitatory neurotransmitter in the mammalian cortex.³⁰³ Glutamate receptors, primarily located in the CNS, are involved in synaptic plasticity, learning, and memory.^{304,305} There are two types of glutamate receptors: metabotropic and ionotropic. Ionotropic glutamate receptors form ion channel pores that allow the nonselective flux of cations upon activation by binding of glutamate.³⁰⁶ Among the ionotropic glutamate receptors, NMDARs, named according to its selective binding of NMDA, have been researched for their role in a range of CNS disorders.³⁰⁷ A majority of NMDARs are tetramers composed of two NR1 subunits, forming the channel, and two NR2A, NR2B, NR2C, or NR2D subunits.³⁰⁸ The physiological and pharmacological properties of NMDARs vary depending on the combination of NR1 and NR2 subunits.³⁰⁹ Under normal conditions, the NMDAR channel is blocked by Mg(II) in a voltage-dependent manner, which can be activated to control the influx of cations [e.g., Na(I), K(I), and Ca(II)].³¹⁰ The depolarization of NMDARs under pathological conditions is proposed to lead to the loss of Mg(II) from the channel, resulting in its overactivation.³¹¹ Dysregulation of NMDAR activation contributes towards the pathology of the disease via cellular Ca(II) dyshomeostasis.^{312,313} Therefore, the modulation of NMDARs has been suggested as a strategy to develop potential therapeutics for CNS-related disorders. Memantine, an uncompetitive NMDAR antagonist for AD treatment approved by the U.S. FDA (Table 1.1), has exhibited its effectiveness in attenuating cognitive decline in moderate to severe AD cases.³¹⁴ The utilization of NMDARs as a target in the past has been challenging due to adverse side effects, a consequence of nonspecific NMDAR recognition.³¹⁵ Nonetheless, the success of memantine has proven its therapeutic potential, and a more specific approach to antagonize NMDARs targeting the neurons affected by AD could be advantageous.³¹⁴ Furthermore, fine-tuning various parameters to inhibit NMDARs through the derivatization of uncompetitive NMDAR antagonists could provide insight into the invention of multifunctional molecules as potential drugs for AD.

Monoamine oxidase (MAOs), a family of enzymes that oxidatively deaminates monoamines, are linked to the pathogenesis of PD since they regulate dopaminergic and serotonergic neurotransmission.^{316–319} The commonalities and correlated onsets between AD and PD have led researchers to investigate the role of MAOs in the pathology of AD. MAOs, found on the outer mitochondrial membrane, are divided into two isoforms, MAO-A and MAO-B, which exhibit overlapping substrate specificities against dopamine, tyramine, and tryptamine.³²⁰ MAO-A, however, is capable of deaminating serotonin, melatonin, norepinephrine, and epinephrine, whereas MAO-B is mainly responsible for breaking down phenethylamine. MAO-catalyzed reactions produce H₂O₂ and ammonia as byproducts.³¹⁶ Thus, the overactivity of MAOs enhances the generation of H₂O₂ possibly leading to oxidative stress.³¹⁶ Inhibition of MAOs has been studied as a promising approach to treat AD.³²¹

Phosphodiesterases (PDEs), composed of 12 families of enzymes responsible for the hydrolysis of cyclic adenosine monophosphate (cAMP) and cyclic guanosine monophosphate (cGMP), play a role in the regulation of intracellular signaling cascades, LTP, and synaptic plasticity.^{322–324} Various members of PDEs have been implicated in a wide range of disorders, including AD and PD.³²² Specifically, the change in the expression of PDE4, PDE7, and PDE8 has been indicated in the AD-affected brain.^{322–324} PDE inhibitors (PDEIs) have been shown to control signaling pathways by elevating the levels of cAMP and cGMP with subsequent activation of the cAMP response element binding (CREB) protein.^{325,326} Such activation of the CREB protein is involved in LTP and synaptic plasticity.^{327,328} Incorporation of the inhibitory activity against specific PDEs in the rational design of multifunctional molecules could be an effective means to construct them into potential drugs for AD. Furthermore, a link between PDEs and tau has been suggested through the direct relation between cAMP and protein kinase A associated with the phosphorylation of tau.^{329,330}

Apolipoprotein E (ApoE) is recognized as a major determinant in lipoprotein metabolism, cholesterol homeostasis, and cardiovascular disease.³³¹ Research regarding the connection between ApoE polymorphisms and AD led to the discovery of ApoE4 as a strong genetic factor.^{332–334} ApoE isoforms (i.e., ApoE2, ApoE3, and ApoE4) have only one or two different amino acid residues; however, they exhibit distinct biological functions.³³⁵ For example, the ApoE4 allele is strongly implicated in sporadic AD, while ApoE2 is observed to be linked to neuroprotection.^{334,336,337}

The direct and indirect relationships between ApoE4 and A β are controversial with research supporting both ApoE's pathological (for ApoE4) and remedial roles (possibly, for ApoE2) in AD. ApoE's effect on A β deposition and neuritic degradation was shown to be specific for the isoform. For example, an increase in the A β burden, fibrillogenesis, and neuritic plaque formation through binding to ApoE4 was greater than that of ApoE3 binding.³³⁸ Hashimoto et al. presented that ApoE increased the levels of A β oligomers in an isoform-dependent manner (ApoE2 < ApoE3 < ApoE4).³³⁹ In addition, ApoE4-expressing astrocytes were indicated to enhance amyloidogenic processing of APP in neurons, and the lack of ApoE4 reduced A β deposition in Tg mice overexpressing human APP^{V717F}.³⁴⁰ On the other hand, Jiang et al. reported the capability of ApoE to promote the proteolytic degradation of A β in an isoformdependent manner, where ApoE4 impaired A β proteolysis, relative to ApoE2 and ApoE3.³⁴¹ Upregulated at the sites of elevated inflammation, ApoE3 and ApoE4 were reported to block glial secretion of TNF α , implying its connection to inflammatory processes.³⁴² Further research to identify ApoE's multifactorial role in AD would be valuable to gain a better understanding to find a direction for developing effective therapeutics. One approach is to inhibit the interactions between ApoE4 and AD pathological factors (e.g., A β) using small molecules. Chen et al. indicated that small molecules able to control the intramolecular interactions between the amino- and carboxyl-terminal domains of ApoE4 could eliminate its detrimental effects in vitro.³⁴³ A recent study displayed a link between ApoE4

and tau pathology, further cementing the involvement of ApoE4 in AD pathogenesis.³⁴⁴ Knock-in of human ApoE4 into a mouse model of tauopathy (1N4R P301S tau) resulted in exacerbated ptau pathology compared to that of ApoE2 and ApoE3, while knockout of ApoE had a protective effect.³⁴⁴ ApoE4/P301S mice further displayed more neurodegeneration and neuroinflammation than ApoE2/P301S and ApoE3/P301S mice, and ApoE knockout mice were once more protected from these pathological changes.³⁴⁴ The isoform-dependent genetic implications of ApoE indicate an aspect of AD in connection to A β and tau, suggesting its therapeutic potential to be considered for the design of multifunctional compounds as possible drug candidates.

Pyroglutamate A β (pGlu-A β) is a variation of A β with an N-terminal pyroglutamate residue implicated for its toxicity.^{345–348} Glutaminyl cyclase is a catalytic enzyme responsible for the pGlu modification of A β .³⁴⁹ Glutaminyl cyclase has been gaining the attention of researchers as a potential therapeutic target for AD due to its upregulation in the areas of the brain affected by AD and its potential contribution toward A β -mediated toxicity.^{346,348–350} Overexpression of glutaminyl cyclase has been shown to induce behavioral deficits in Tg mice, whereas glutaminyl cyclase knockout improved the behavioral phenotype in 5xFAD mice.³⁴⁶ Increasing evidence supporting the effectiveness of inhibiting glutaminyl cyclase implies a tactic that could be valuable to consider in the design of multifunctional molecules as potential therapeutics.^{348,350,351}

Neuroinflammation is a biological response of the nervous tissue initiated in reaction to detriments (e.g., infection and traumatic brain injury).³⁵² Pathological events of AD, including A β accumulation and tau hyperphosphorylation, are reported to invoke inflammatory responses in vulnerable regions of the AD-affected brain.³⁵³ Gliosis and activated glial cells are two major histopathological signs of neuroinflammation in AD.³⁵³ Previous studies suggest that the direct and indirect damage from inflammation may exacerbate the pathological processes through a positive feedback loop.³⁵³ The interconnected inflammation pathways can be activated by A β aggregates³⁵⁴ and NFTs³⁵⁵ through classical and alternative complement pathways.³⁵³

1.3. Conclusions

Multiple aspects of AD presented thus far represent a large portion of the research effort devoted toward determining the factors responsible for neurodegeneration observed in AD. Although a great deal of work has been dedicated to the cause, it is still unclear if the pathological elements mainly indicated in the AD-affected brain serve as causative factors of the disease or are the products of unidentified upstream events. The number of potential pathological components [e.g., peroxisome proliferator activator receptor γ (PPAR γ),^{356,357} phospholipase A2 (PLA2s),^{358,359} cyclophilin D (CypD),^{360,361} GD3 synthase,³⁶² plasminogen activator,^{363,364} dickkopf1 (DKK1),³⁶⁵ calpain,^{366,367} and histone deacetylases (HDACs)³⁶⁸], speculated to play a role in AD pathology, represent the gap between our understanding

of the disease and its complexity. On the basis of diverse potential pathological targets and their suggested interconnections towards the pathogenesis of AD, the development of chemical tools would be valuable for understanding and modifying pathogenic factors in neurodegenerative diseases.

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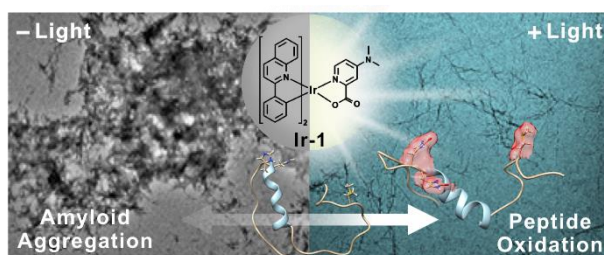
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Chapter 2.

An Iridium(III) Complex as a Photoactivatable Tool for Oxidation of Amyloidogenic Peptides with Subsequent Modulation of Peptide Aggregation



The results and discussion presented in this chapter were reported in the publication [Kang, J.;[†] Lee, S. J. C.;[†] Nam, J. S.;[†] Lee, H. J.; Kang, M.-G.; Korshavn, K. J.; Kim, H.-T.; Cho, J.; Ramamoorthy, A.; Rhee, H.-W.; Kwon, T.-H.; Lim, M. H. *Chem. Eur. J.* **2017**, 23, 1645–1653 ([†]equal contribution)]. Professor Tae-Hyuk Kwon, Jung Seung Nam, and Hyun-Tak Kim prepared **Ir-1** and measured its photophysical properties with data analysis. Professor Ayyalusamy Ramamoorthy and Dr. Kyle J. Korshavn carried out the studies of 2D HMQC NMR. Dr. Shin Jung C. Lee and I performed the mass spectrometric investigations with data analysis, and Professor Hyun-Woo Rhee and Myeong-Gyun Kang conducted in-gel digestion studies. I conducted gel/Western blot and TEM with data analysis. I, Dr. Shin Jung C. Lee, and Dr. Hyuck Jin Lee wrote the manuscript under the assistance of Professor Mi Hee Lim.

2.1. Introduction

Amyloidogenic peptides are found in human degenerative diseases [e.g., amyloid- β (A β) for Alzheimer's disease (AD), α -synuclein (α -Syn) for Parkinson's disease (PD), and human islet amyloid polypeptide (hIAPP) for type II diabetes].^{1–6} Amyloidogenic peptides have aggregate-prone properties to form β -strand fibrils through oligomeric conformations, and their aggregation has been suggested to be linked to the pathogenesis of degenerative disorders.^{1–6} Thus, a variety of approaches have been developed to regulate or suppress the aggregation pathways of amyloidogenic peptides.^{2,7–12} Among such methods, peptide modifications, including peptide oxidation, have been recently implicated as a strategy suitable for modulation of amyloidogenic peptide aggregation (Figure 2.1a).^{13–23}

To trigger the oxidation of peptides, some chemical reagents, such as metal ions, have been utilized.^{14,24–27} Metal ions are frequently used for peptide oxidation; however, they require harsh additional oxidants.^{14,24–27} In addition, chemical reagents capable of generating oxidants from O₂ upon photoactivation have been developed for use as photosensitizers in various fields because light is a readily accessible resource.^{13,28–40} A series of organic molecules, such as riboflavin, rose bengal, methylene blue, and porphyrins, have been used as photoinduced reagents,^{13,29–35} however, (i) many of them have relatively lower quantum yields than those of photoactivatable transition-metal complexes;^{41–44} and (ii) some organic agents are less stable, which potentially indicates their degradation upon irradiation.^{28,36} Photoactivatable metal complexes present relatively high quantum yields, structural stability, and tunable geometries and properties upon ligand substitution.^{28,36} Due to these beneficial aspects, multiple metal complexes have been designed and mediated for photoinduced oxidation of peptides.^{37–40} One inorganic complex, [Ru(bpy)₃]²⁺ (bpy = 2,2'-bipyridine), has been frequently employed for oxidative modifications of peptides through light exposure.^{38–40} To achieve peptide oxidation, this ruthenium(II) complex still needs an additional electron acceptor (e.g., ammonium persulfate), however, which could lead to cytotoxicity and limit its applications.^{38–40,45} Thus, robust inorganic complexes able to efficiently oxidize peptides simply by light introduction without the assistance of harsh additives would be of significant value for gaining a greater understanding of peptide-related chemistry and biology.

Herein, we report an iridium(III) complex, **Ir-1** (Figure 2.1b), as a chemical tool for the oxidation of amyloidogenic peptides with the subsequent control of their aggregation under mild conditions that only include readily available O₂ and visible light. **Ir-1** was rationally designed as such a tool through incorporating the general properties of Ir(III) complexes previously reported for various applications, including photoactivation, formation of reactive oxygen species (ROS) upon light exposure, and relatively stable octahedral geometry, as well as relatively easy introduction of a ligand containing a structural moiety, suggested to be important for interactions with amyloidogenic peptides, on the Ir(III)

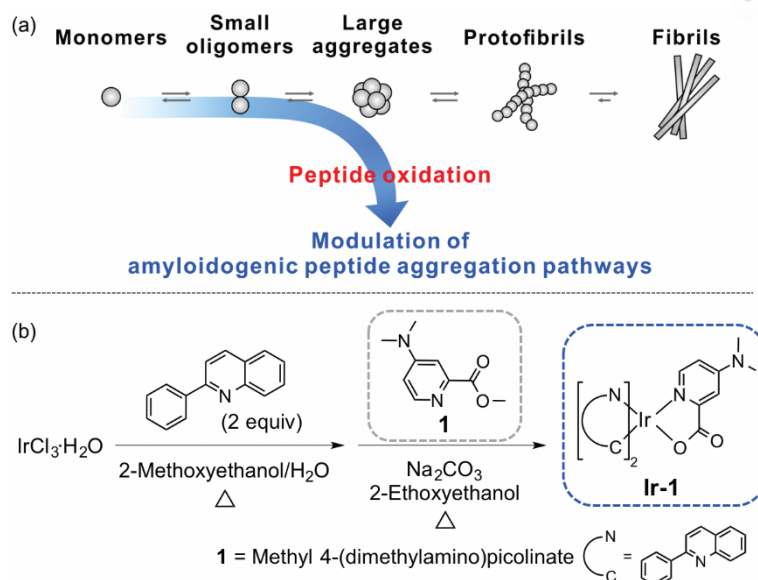


Figure 2.1. Schematic description of amyloidogenic peptide aggregation and chemical structures of **Ir-1** and **1**. As shown in (a), oxidation of amyloidogenic peptides could control their aggregation pathways. (b) Synthetic routes to **Ir-1**.

center.^{28,46–53} Representative amyloidogenic peptides (i.e., A β , α -Syn, and hIAPP) were indicated to be noticeably oxidized upon treatment of **Ir-1** with photoactivation under aerobic conditions, as monitored by electrospray ionization mass spectrometry (ESI-MS), and their oxidation sites (as potential sites, methionine, histidine, and tyrosine residues) were identified by tandem MS (ESI-MS²). Even with oxidative modifications of a few residues in these amyloidogenic peptides, the aggregation pathways were noticeably modulated, resulting in distinct morphological features (e.g., smaller-sized or amorphous peptide species, instead of fibrils). Taken together, our rational design and investigations into **Ir-1** illustrate the potential of transition metal complexes as chemical tools for the oxidative modification of amyloidogenic peptides simply by employing light and O₂. In addition, our studies corroborate that small changes in amyloidogenic peptides, such as oxidation at a few specific residues, are able to transform overall peptide aggregation pathways; this suggests novel and viable directions for amyloid management (Figure 2.1a).

2.2. Results and Discussion

2.2.1. Rational Design of Ir-1 for Oxidation of Amyloidogenic Peptides

For the oxidation of amyloidogenic peptides simply upon photoactivation under mild conditions, **Ir-1** (Figure 2.1b) was rationally designed as a chemical tool by taking into account the characteristics found in previously reported photoactivatable Ir(III) complexes, as well as specificity for amyloidogenic peptides: (i) photoproperties with relatively low-energy radiation (i.e., visible light);^{49,50} (ii) the ability to produce ROS [e.g., singlet oxygen (¹O₂)] from redundant O₂, which is responsible for peptide oxidation, upon photoactivation;^{28,48} (iii) robust octahedral coordination, which can provide relative

structural stability without any structural modifications when light is introduced;⁴⁸ (iv) strong spin-orbit coupling of the Ir(III) center, which could facilitate electronic transitions without the assistance of additional electron acceptors;^{49,50} and (v) incorporation of a ligand (**1**) containing a dimethylamino group, suggested to be crucial for interactions with amyloidogenic peptides,^{46,47} onto the Ir(III) center (Figure 2.1b).

Ir-1 was obtained in relatively high yield (ca. 80%) through previously known two-step procedures with slight modifications, as depicted in Figure 2.1b.⁵⁴ Moreover, **Ir-1** is easily photoactivatable under mild conditions [e.g., excitation with visible light { ϵ (463 nm) = $5.78 (\pm 0.12) \times 10^3 \text{ M}^{-1} \text{ cm}^{-1}$; Table 2.1} and aerobic conditions] as shown by its quantum yield for phosphorescence [$\Phi_p = 0.41 (\pm 0.02)$; Table 2.1]. The ability of **Ir-1** to generate singlet oxygen ($^1\text{O}_2$) from triplet dioxygen ($^3\text{O}_2$) was also confirmed by determining the quantum yield of $^1\text{O}_2$ [$\Phi_s = 0.25 (\pm 0.03)$; Table 2.1]. Overall, an octahedral Ir(III) complex, **Ir-1**, was constructed as a photoactivatable tool to oxidize amyloidogenic peptides without the need for harsh conditions through relatively easy synthetic routes with a high yield, and demonstrated to generate oxidants (i.e., $^1\text{O}_2$) from readily accessible O_2 .

Table 2.1. Photophysical properties of **Ir-1**.

	Ir-1
$\lambda_{\text{ex, max}}$ (nm)	463
$\lambda_{\text{em, max}}$ (nm)	600
ϵ [$\text{M}^{-1} \text{cm}^{-1}$; 463 nm; in H_2O (1% v/v DMSO)]	$5.78 (\pm 0.12) \times 10^3$
Lifetime (ns)	238
Φ_p	$0.41 (\pm 0.02)$
Φ_s	$0.25 (\pm 0.03)$

2.2.2. Oxidative Modifications of Amyloidogenic Peptides by Ir-1

To investigate whether the oxidation of amyloidogenic peptides by **Ir-1** under aerobic conditions would occur with light activation, three amyloidogenic peptides (i.e., A β , α -Syn, and hIAPP found in AD, PD, and type II diabetes, respectively) were chosen as representative amyloidogenic peptides, and the resultant monomeric peptide species upon treatment with **Ir-1** were first monitored by means of ESI-MS (Figure 2.2). These three amyloidogenic peptides were observed to be oxidized with the addition of lightactivated **Ir-1** under aerobic conditions. Without light, even in the presence of **Ir-1**, all amyloidogenic peptides were in nonoxidized forms (Figure 2.2, middle, gray). In the case of A β_{40} , the oxidized A β monomers had a 16 Da increase in mass from nonoxidized peptides; this implied the

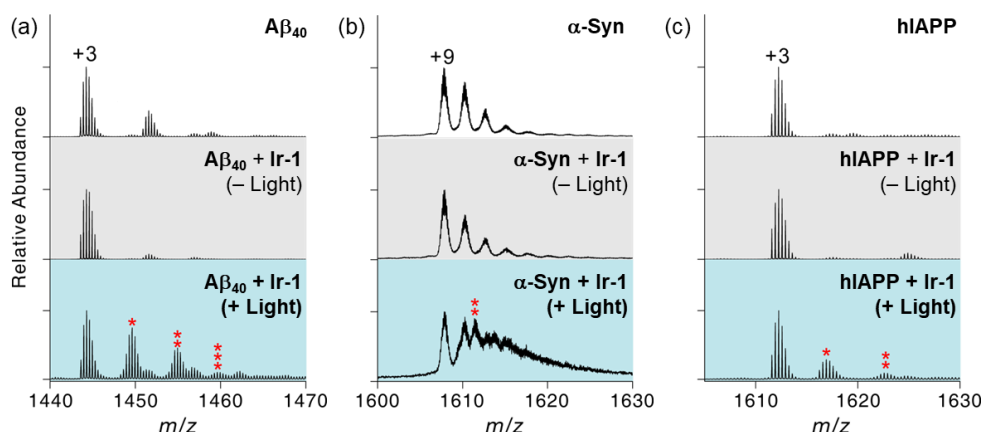


Figure 2.2. Oxidation of amyloidogenic peptides by **Ir-1** upon light activation. Mass spectrometric analyses of amyloidogenic peptides [(a) $A\beta_{40}$, (b) α -Syn, and (c) hIAPP] upon treatment with **Ir-1** in the presence of light. Oxidized peptide ions are indicated with red asterisks, and the number of asterisks indicates the number of oxygen atoms incorporated into the peptides. Conditions: [peptide] = 100 μ M; [**Ir-1**] = 500 μ M; pH 7.4; 37 $^{\circ}$ C; 1 h; no agitation; 1 sun light for 10 min (for samples treated with light); aerobic conditions. Details for the assignment of oxidized peaks are included in the Experimental Section.

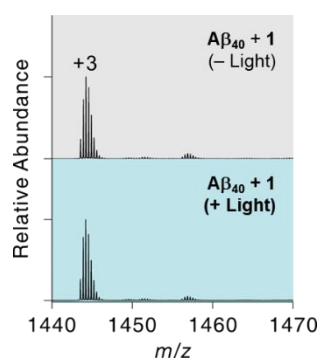


Figure 2.3. ESI-MS spectra for $A\beta_{40}$ with **1** in the absence (top) and presence (bottom) of light. Conditions: [$A\beta_{40}$] = 100 μ M; [**1**] = 500 μ M; pH 7.4; 37 $^{\circ}$ C; 1 h; no agitation; 1 sun light for 10 min (for the samples treated with light); aerobic conditions.

incorporation of one oxygen atom into the peptide (Figure 2.2a, bottom, blue). Notably, ligand **1** alone was not able to oxidize $A\beta_{40}$ (Figure 2.3). Similar to $A\beta_{40}$, doubly oxidized α -Syn with a 32 Da increase in mass, relative to that of the native peptide, was indicated; this suggested the introduction of two oxygen atoms into the peptide (Figure 2.2b, bottom, blue). Slightly different from both $A\beta$ and α -Syn, singly oxidized monomeric hIAPP presented a 14 Da difference in mass from nonoxidized peptides (Figure 2.2c, bottom, blue). A 14 Da increase in mass could result from the addition of one oxygen atom to hIAPP, along with deprotonation.^{13,33,55}

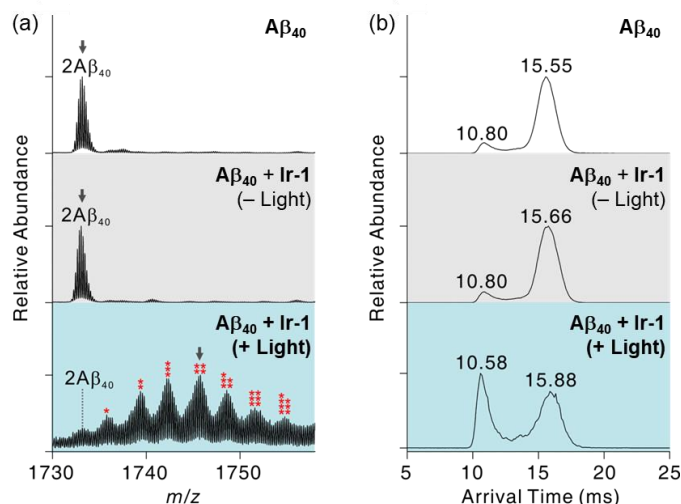


Figure 2.4. Oxidation of $A\beta_{40}$ dimers by **Ir-1** upon photoactivation. (a) ESI-MS spectra for +5-charged dimers with **Ir-1** in the absence and presence of light. The oxidized dimers are only detected by **Ir-1** with light exposure (bottom, blue). The number of red asterisks indicates the number of oxygen atoms incorporated into $A\beta_{40}$ dimers. (b) ATDs for nonoxidized (top and middle) and tetraoxidized dimers (bottom). Each ion selected for IM-MS analysis is indicated with gray arrows in (a). The oxidized dimer incorporated with four oxygen atoms presents the higher abundance in the distribution with short drift time (bottom) than that of nonoxidized $A\beta_{40}$ (top and middle), which implies that structural compaction can be induced by oxidation. Conditions: $[A\beta_{40}] = 100 \mu M$; $[Ir-1] = 500 \mu M$; pH 7.4; 37 °C; 1 h; no agitation; 1 sun light for 10 min (for samples treated with light); aerobic conditions.

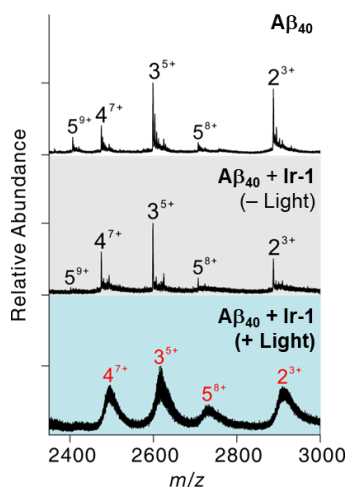


Figure 2.5. ESI-MS spectra for oligomeric $A\beta_{40}$ with **Ir-1** in the absence and presence of light. The + z -charged n -mer is denoted as n^{z+} . Peak annotations for oxidized oligomers are highlighted in red. Conditions: $[A\beta_{40}] = 100 \mu M$; $[Ir-1] = 500 \mu M$; pH 7.4; 37 °C; 1 h; no agitation; 1 sun light for 10 min (for the samples treated with light); aerobic conditions.

Second, we examined whether amyloidogenic peptide oligomers (focusing on $A\beta$ oligomers) by **Ir-1** could be oxidized with light activation under aerobic conditions. From the samples containing $A\beta$

and **Ir-1** upon exposure to light and O₂, the oxidation of both dimers and larger oligomers was revealed (Figures 2.4a and 2.5). As demonstrated in Figure 2.4a, multiple oxygen atoms (e.g., for dimers, up to seven oxygen atoms) were indicated to be incorporated into the oxidized oligomers.

Moreover, structural changes to monomeric and oligomeric peptide species accompanied by oxidation were probed by means of ion mobility mass spectrometry (IM-MS), which enabled to characterize conformations based on the mobility of ions passing through a cell filled with neutral gas.⁵⁶ In the case of A β monomers, there was no remarkable difference in arrival time distributions (ATDs) between singly oxidized and nonoxidized A β ₄₀ monomers (Figure 2.6). Distinguishable from A β monomers, a change in the IM-MS data of A β ₄₀ dimers upon oxidation was presented at two dominant ATDs, centered at 10.80 and 15.55 ms, respectively (Figure 2.4b). Nonoxidized A β ₄₀ dimers exhibited greater dominance in the larger ATD, whereas the oxidized dimers had the opposite tendency, which suggested that peptide oxidation could lead to structural compaction in the dimers. Although structural details of oxidized dimers have not been elucidated, their structural compaction might assist in modulating peptide aggregation because previous studies indicated that conformationally compact A β species could alter peptide aggregation pathways to form amorphous aggregates.^{8–11}

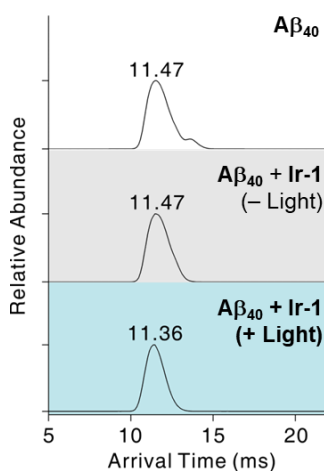


Figure 2.6. IM-MS spectra for +3-charged A β ₄₀ monomers. ATD for nonoxidized (top and middle) and singly oxidized monomeric A β ₄₀ (bottom). There is no significant difference between ATD of nonoxidized A β ₄₀ (top and middle) and that of singly oxidized A β ₄₀ upon addition of **Ir-1** in the presence of light (bottom).

Furthermore, the oxidation of a nonamyloidogenic structured protein, ubiquitin, was also investigated when **Ir-1** was added with light under aerobic conditions. Ubiquitin was selected as an archetypal structured protein because all secondary structures (e.g., α -helix, β -strand, and random coil) could be found in ubiquitin.⁵⁷ Ubiquitin treated with **Ir-1** was shown to be oxidized with light exposure under aerobic conditions (Figure 2.7, bottom, blue); however, oxidized ubiquitin was significantly less abundant than the oxidized forms of intrinsically disordered amyloidogenic peptides (i.e., A β ₄₀, α -Syn,

and hIAPP). Overall, oxidative modifications of amyloidogenic peptides, lacking ordered structures, are more readily achieved over structured peptides by **Ir-1** under mild conditions, including light and O₂, which could direct structural compaction; this supports the utilization of **Ir-1** as a photoactivatable tool for the oxidation of amyloidogenic peptides.

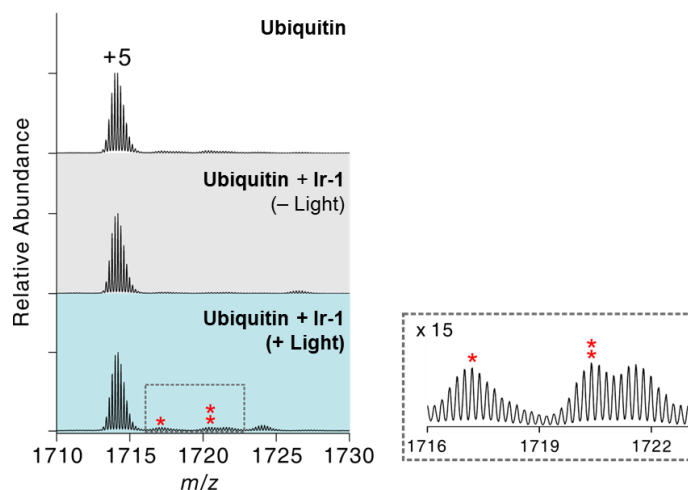


Figure 2.7. ESI-MS spectra for ubiquitin with **Ir-1** in the absence and presence of light. The number of red asterisks indicates the number of the oxygen atoms incorporated into the peptide. The oxidized ubiquitin peaks are magnified and indicated in the dotted box. Conditions: [ubiquitin] = 100 μ M; [**Ir-1**] = 500 μ M; pH 7.4; 37 $^{\circ}$ C; 1 h; no agitation; 1 sun light for 10 min (for the samples treated with light); aerobic conditions.

2.2.3. Identification of Oxidation Sites in Amyloidogenic Peptides

The resultant oxidized amyloidogenic peptides, produced by the addition of **Ir-1** with light exposure under aerobic conditions, were further studied by ESI-MS² to determine the oxidation sites in the peptides.^{10,11} The fragment ions generated by selectively applying collisional energy to the singly and doubly oxidized amyloidogenic peptides were analyzed (Figure 2.8). First, the oxidation sites in A β ₄₀ were identified. The singly oxidized fragments, highlighted in red, were observed in *b* fragments, which were cleaved from the N-terminus (Figure 2.8b). All *b* fragments smaller than *b*₁₃ existed as nonoxidized forms, whereas those larger than *b*₃₄ represented only oxidized fragments. Methionine 35 (M35) is known to be the most readily oxidizable amino acid in A β .²² If oxidation occurred only at M35, all fragments smaller than *b*₃₅ would not be oxidized (Figure 2.8a); however, oxidized *b* fragments were indicated to be smaller than *b*₃₅, which implied the existence of other oxidation sites (Figure 2.8b). Based on previously reported studies, other possible oxidation sites could be histidine residues (i.e., H13, H14).^{26,59} In the ESI-MS² spectrum for doubly oxidized A β ₄₀, there was no oxidized fragment smaller than *b*₁₃ (Figure 2.8d). Because fragments from *b*₁₃ to *b*₃₄ only existed in singly oxidized forms (highlighted in red in Figure 2.8), this region would include one oxidation site, possibly H13 or H14.

All fragments larger than b_{34} were doubly oxidized (denoted in green), which implied the incorporation of one oxygen atom into M35 to generate a sulfoxide form (Figure 2.8c and d).

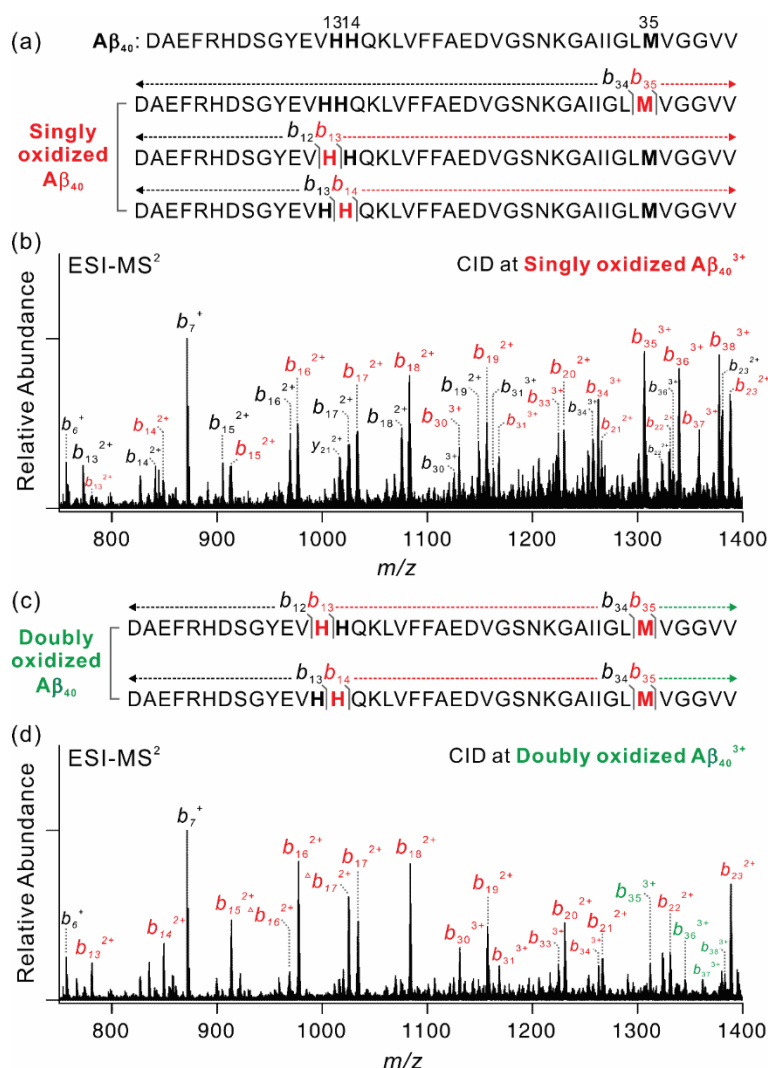


Figure 2.8. Identification of the oxidation sites in $A\beta_{40}$. (a and c) The peptide sequence and annotation for ESI-MS² and (b and d) ESI-MS² spectra for singly and doubly oxidized $A\beta_{40}$. Singly and doubly oxidized b fragments (N-terminal fragment ions) or y fragments (C-terminal fragment ions) are denoted in red and green, respectively. The peaks assigned as triangles (b_{16} and b_{17}) indicate that the loss of a water molecule occurs at serine, threonine, glutamate, or aspartate residues in these fragment ions.⁵⁸

For further analysis of the oxidation sites in $A\beta$, $A\beta_{40}$ treated with **Ir-1** in the absence and presence of light was evaluated by 2D band-selective optimized flip-angle short transient heteronuclear multiple quantum correlation (SOFAS-T-HMQC) NMR spectroscopy (Figures 2.9). In the absence of light, minimal chemical shift perturbations (CSPs) of uniformly ¹⁵N-labeled $A\beta_{40}$ appeared upon incubation with **Ir-1** (Figure 2.9c), which implied no significant interaction of **Ir-1** with the peptide. Following exposure of the $A\beta$ samples containing **Ir-1** to light, a dramatic increase in the CSPs at V12, D23, and M35 was observed (Figure 2.9d). A noticeable change in the CSP of M35 suggests that there

are interactions near M35, which is consistent with observation monitored by ESI-MS². In the case of histidine residues, although they were not well resolved within the spectra due to peak overlap, the enhanced CSP of V12, proximately located to H13 or H14, could be expected, which proposed oxidative modifications at H13 or H14, as shown in our ESI-MS² studies. Notably, in the NMR spectra, D23 was adjacent to M35 with some overlap, so the shift of M35 might affect its CSP. Thus, our NMR data support that A β ₄₀ is oxidized at specific sites (potentially, M35, H13, and H14) by **Ir-1** upon light stimulation under aerobic conditions.

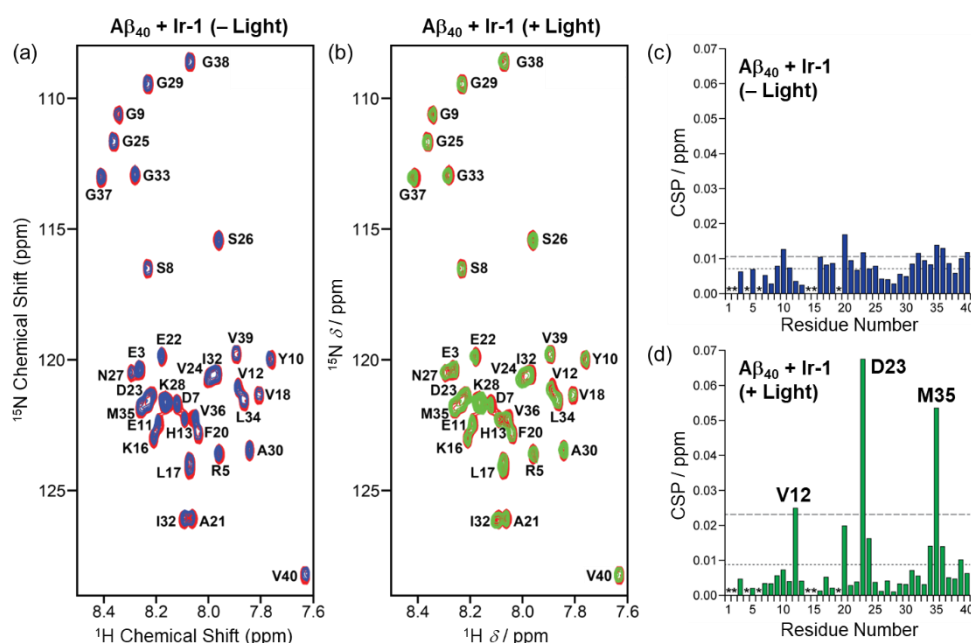


Figure 2.9. SOFAST-HMQC NMR studies of uniformly ¹⁵N-labeled A β ₄₀ monomer upon treatment with **Ir-1** with and without light. (c and d) The chemical shift perturbations (CSPs) for each spectrum [in the (a) absence or (b) presence of light], relative to the spectrum of A β ₄₀ without **Ir-1**, were calculated. Conditions: [¹⁵N-labeled A β ₄₀] = 80 μ M; [**Ir-1**] = 160 μ M; pH 7.4; 37 $^{\circ}$ C; ambient light for 1 h (for samples treated with light); aerobic conditions. *Residues could not be resolved for analysis.

Potential oxidation sites in the other amyloidogenic peptides (i.e., α -Syn and hIAPP), when treated with **Ir-1** in the presence of light under aerobic conditions, were also investigated by means of ESI-MS² (Figure 2.10). When the collisional energy was applied at doubly oxidized α -Syn (Figure 2.10a and b), no oxidation was found in small N-terminal fragments; this reflects that oxidation at M1 and M5 rarely occurs. The C-terminal fragment y_{13} was detected in a nonoxidized form, but b_{119} was present in both oxidized and nonoxidized forms. One oxidation site existed between P120 and M127, and the most plausible location was M127. Since singly oxidized b_{116} and b_{119} ions were relatively abundant, M116 was also estimated to be possibly oxidized. There were oxidized fragments smaller than b_{116} , such as b_{63} , b_{65} , and b_{66} , which implied that there were oxidation sites other than M116 and

Previous studies proposed that methionine, histidine, and tyrosine residues in amyloidogenic peptides were susceptible to oxidative modification, which could affect their aggregation behavior.^{17,20,22,60} Particularly, oxidative modifications of methionine residues have been reported to inhibit β -strand formation of amyloidogenic peptides.^{20,22,60} Incorporation of oxygen atoms into methionine residues could provide partial negative charges and further enhance the polarity of peptides.^{15,20,60} In the case of A β , the increased polarity of oxidized M35 could reduce hydrophobic contacts in the C-terminal region and destabilize a β -strand structure in which M35 proximately interacts with the aromatic ring of F19.^{20,60} Along with a change in polarity, greater structural disorder and reduced helicity were also found in methionine-oxidized α -Syn.^{15,61} Specifically, oxidation at M116 and M127 presumably disrupts α -Syn aggregation because these residues are suggested to mediate long-range interactions with the central hydrophobic regions.⁶² Other important oxidation sites are histidine residues. Due to its structural features, such as an imidazole ring and two protonation states, histidine has versatile roles in multiple interactions (e.g., cationic- π interactions, π - π stacking, hydrogen- π interactions, coordination, and hydrogen bonding).⁶³ Depending on pH, histidine can present different protonation states that have effects on the molecular behavior of amyloidogenic peptides, including aggregation, through alteration of the strength of interactions.^{63,64} In addition, histidine is known as a metal binding site in amyloidogenic peptides.⁶⁵⁻⁶⁹ Binding of metal ions [e.g., Cu(II), Zn(II)] to peptides is shown to accelerate amyloidogenic peptide aggregation or induce the formation and stabilization of toxic oligomeric aggregates.^{2,66,67,70} Upon the formation of 2-oxo-histidine, metal binding affinities were reported to be substantially decreased; thus, oxidative modifications of histidine residues might destabilize complexes of amyloidogenic peptides with metal ions.^{69,71} Collectively, methionine, histidine, and/or tyrosine residues, the potential oxidation sites of A β , α -Syn, or hIAPP, which were suggested to be essential for the properties and aggregation of these amyloidogenic peptides, were indicated by our MS and NMR studies. Oxidative modifications are present at a few specific residues in amyloidogenic peptides, which might be able to modulate their aggregation pathways potentially through altering intra- or intermolecular interactions critical for β -strand formation (see below).

2.2.4. Aggregation Behavior Influenced upon Oxidation of Amyloidogenic Peptides by Light-Activated Ir-1

2.2.4.1. Change in the Size Distribution

To investigate whether peptide oxidation could transmute the aggregation of amyloidogenic peptides, two inhibition (Figures 2.11a and 2.12a) and disaggregation (Figure 2.13a) experiments⁸⁻¹¹ were carried out mainly with A β (two major isoforms, A β ₄₀ and A β ₄₂). Size distributions of the resultant A β ₄₀ and

A β_{42} species treated with **Ir-1** were evaluated by gel electrophoresis with Western blotting (gel/Western blot) by using an anti-A β antibody (6E10).

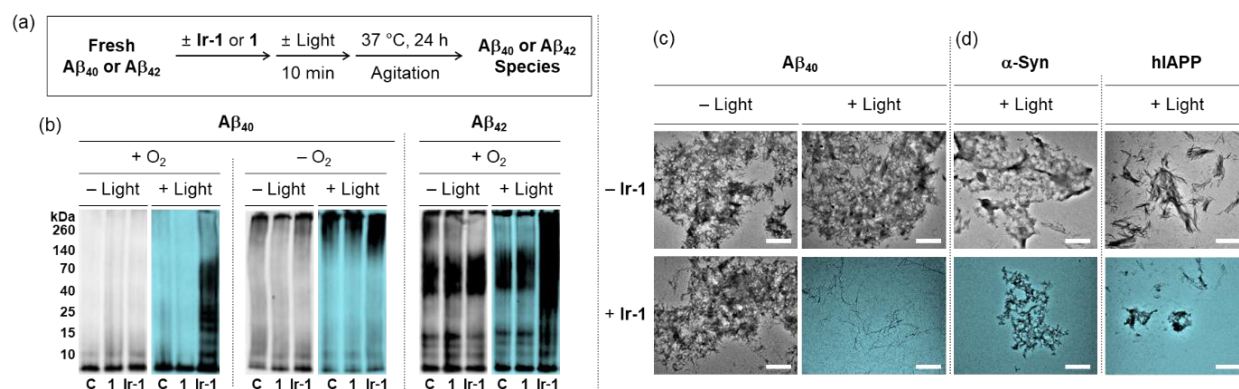


Figure 2.11. Effects of **Ir-1** and **1** on peptide aggregation pathways. (a) Scheme of the inhibition experiments. (b) Analyses of the resultant A β_{40} and A β_{42} species generated from various conditions [aerobic (left) and anaerobic (right) conditions] by gel/Western blot with an anti-A β antibody (6E10). Lanes: (C) A β_{40} or A β_{42} ; (1) A β_{40} or A β_{42} + **1**; (Ir-1) A β_{40} or A β_{42} + **Ir-1**. (c and d) TEM images of the samples from (b) and the light-treated samples containing α -Syn or hIAPP with and without **Ir-1** (scale bar = 1 μ m). Conditions: [peptide] = 25 μ M; [**Ir-1** or **1**] = 50 μ M; pH 7.4; 37 °C; 24 h; constant agitation; 1 sun light for 10 min (for samples treated with light).

In the inhibition studies (Figure 2.11a), when fresh A β_{40} was incubated with **Ir-1** in the presence of light under aerobic conditions, various molecular weights (MWs) of peptide species were visualized in the gel/Western blot (Figure 2.11b, left). Distinct from the result with light exposure, **Ir-1** could not generate diverse sizes of A β aggregates without light. In addition, when the ligands, **1** and 2-phenylquinoline (Figure 2.1b), were not coordinated to the Ir(III) center, they had no noticeable effect on A β aggregation, even with light under aerobic conditions (Figures 2.11b and 2.12). When **Ir-1** was incubated with fresh A β_{42} , similar reactivity trends were presented to those with A β_{40} (Figure 2.11b, right). Diverse MW distributions of A β_{42} species were shown with both **Ir-1** and light. Furthermore, the inhibition experiments were conducted in the absence of O₂ to verify if A β aggregation could be influenced upon oxidation of peptides by oxidants generated by O₂ with light-activated **Ir-1**. A β aggregation pathways were not indicated to be varied under anaerobic conditions, even in the presence of light (Figure 2.11b, middle).

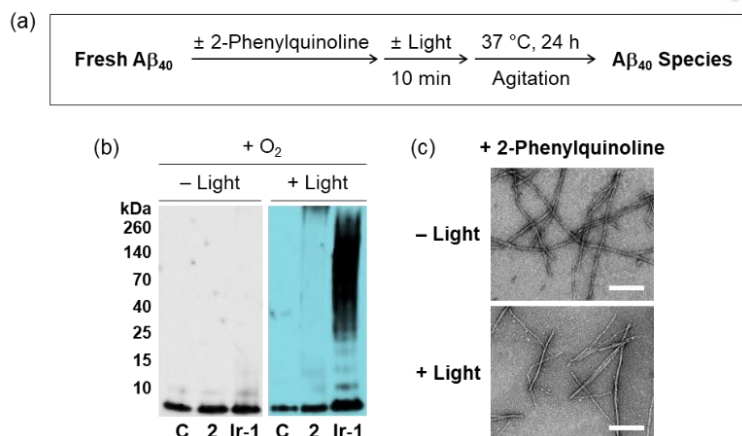


Figure 2.12. Effect of the ligand (2-phenylquinoline, Figure 2.1) on Aβ₄₀ aggregation. (a) Scheme of the inhibition experiment. (b) Analysis of the resultant Aβ₄₀ species visualized by gel/Western blot with an anti-Aβ antibody (6E10). Lanes: (C) Aβ₄₀; (2) Aβ₄₀ + 2-phenylquinoline; (Ir-1) Aβ₄₀ + **Ir-1**. (c) TEM images of the samples from (b) (scale bar = 200 nm). Conditions: [Aβ₄₀] = 25 μM; [2-phenylquinoline or **Ir-1**] = 50 μM; pH 7.4; 37 °C; 24 h; constant agitation; 1 sun light for 10 min (for the samples treated with light).

Moreover, in order to disassemble preformed Aβ₄₀ aggregates or redirect their further aggregation upon oxidation with **Ir-1** in the presence of light and O₂, the disaggregation experiment was carried out (Figure 2.13). Similar to the inhibition studies, preformed Aβ₄₀ aggregates were observed with a wide range of sizes only after treatment with **Ir-1** upon light exposure in the presence of O₂. Overall, our gel/Western blot results from both inhibition and disaggregation experiments suggest that 1) **Ir-1** is able to transmute Aβ aggregation pathways only with light activation under aerobic conditions; and 2) the overall structure of **Ir-1** over individual structural components (e.g., ligand **1**) is essential to alter Aβ aggregation in the presence of both light and O₂. Combining the results with the control of light and O₂, it is demonstrated that Aβ oxidation, triggered by photoactivated **Ir-1** with O₂, could direct the modulation of peptide aggregation pathways.

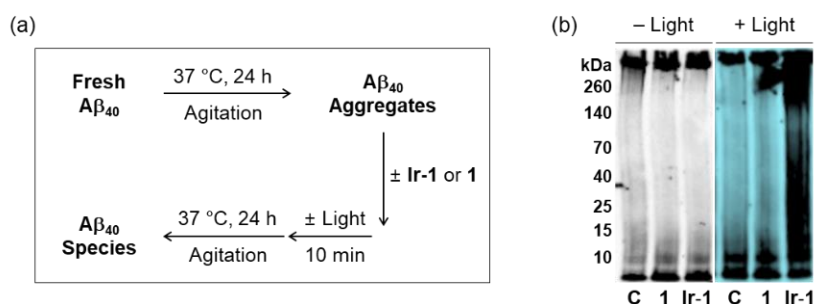


Figure 2.13. Effects of **Ir-1** and **1** on the disassembly of preformed Aβ₄₀ aggregates. (a) Scheme of the disaggregation experiment. (b) Analysis of the resultant Aβ₄₀ species was visualized by gel/Western blot with an anti-Aβ antibody (6E10). Conditions: [Aβ₄₀] = 25 μM; [**Ir-1** or **1**] = 50 μM; pH 7.4; 37 °C; 24 h; constant agitation; 1 sun light for 10 min (for the samples treated with light); aerobic conditions. Lanes: (C) Aβ₄₀; (1) Aβ₄₀ + **1**; (Ir-1) Aβ₄₀ + **Ir-1**.

2.2.4.2. Morphological Changes of Amyloidogenic Peptides

The degree of regulating the aggregation pathways of amyloidogenic peptides was also monitored through morphological changes visualized by transmission electron microscopy (TEM) (Figure 2.11c and d). From the TEM analyses, the resultant peptides upon treatment with both **Ir-1** and light under aerobic conditions were observed to be smaller, while either structured fibrils or large aggregates were indicated without light. In the case of A β ₄₀, the treatment of the peptide with **Ir-1** induced the formation of short and thin fibrils in the presence of both light and O₂ (Figure 2.11c). Additionally, the morphologies of α -Syn and hIAPP were also transformed to smaller amorphous aggregates when **Ir-1** was added with exposure of both light and O₂, instead of large aggregates or fibrils produced in the absence of **Ir-1** (Figure 2.11d). Therefore, along with the gel/Western blot data, our TEM studies imply that the aggregation of amyloidogenic peptides could be transfigured upon treatment with light-activated **Ir-1** under aerobic conditions.

2.3. Conclusions

Several strategies for understanding and suppressing the aggregation of amyloidogenic peptides, found in amyloid-related disorders and suggested to be linked to their pathogenesis, have been developed. One of the tactics would be related to oxidative modifications of the amino acid residues essential for properties and aggregation behaviors of peptides. For the oxidation of amyloidogenic peptides, an inorganic complex, **Ir-1**, was rationally designed to be a chemical tool that has a relatively stable framework and is capable of generating oxidants (e.g., ¹O₂) from readily accessible O₂ simply upon photoactivation employing low-energy radiation.

On the basis of our biochemical and biophysical analyses, **Ir-1** is shown to significantly induce oxidative modifications of amyloidogenic peptides, such as A β , α -Syn, and hIAPP, followed by alteration of their aggregation pathways. Peptide oxidation by photoactivated **Ir-1** is more noticeable for amyloidogenic peptides over well-structured nonamyloidogenic peptides. By MS and NMR, the oxidation sites are indicated to be potentially located at methionine, histidine, and/or tyrosine residues in these amyloidogenic peptides. Through minor alterations at a few specific residues in peptides by photoactivated **Ir-1** under mild conditions, their aggregation pathways can be modulated. Overall, our rational design and fundamental investigations of **Ir-1** demonstrate the promise of an inorganic complex in being developed as a chemical tool for oxidative modifications of amyloidogenic peptides with the subsequent control of their aggregation. Such a tool will assist in advancing our fundamental understanding towards amyloidogenic peptides, as well as providing insight into developing effective approaches for amyloid management.

2.4. Experimental Section

2.4.1. Materials and Methods

All reagents were purchased from commercial suppliers and used as received, unless otherwise noted. Compound **1** (**1** = methyl 4-(dimethylamino)picolinate)⁷² and the cyclometalated chloridebridged Ir(III) dimer ($[\text{Ir}(\text{C}^{\wedge}\text{N})_2(\mu\text{-Cl})_2]$)⁷³ were prepared by following previously reported procedures. The prepared **Ir-1** was characterized by NMR, FTIR, HRMS, and elemental analyzer on an Agilent 400-MR DD2 NMR spectrometer, Varian Cary 620/670 FTIR spectrometer (UNIST Central Research Facilities, Ulsan, Republic of Korea), Bruker maXis™ HD Ultra-high resolution Q-TOF LC MS/MS system (HRMS; The Cooperative Laboratory Center of Pukyong National University, Busan, Republic of Korea), and Thermo Flash 2000 (UNIST Central Research Facilities, Ulsan, Republic of Korea), respectively. A β ₄₀ and A β ₄₂ were purchased from Anygen (A β ₄₀ = DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV, A β ₄₂ = DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA; Nammyun, Jangseong-gun, Republic of Korea). α -Syn and hIAPP were obtained from Anaspec and Peptron, respectively [α -Syn = MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTKEQVTNVGGAVVTGVTAVAQKTVEGAGSIAAATGFVKKDQLGKNEEGA PQEGILEDMPVDPDNEAYEMPSEEGYQDYEP (Fremont, CA, USA); hIAPP = KCNTATCATQRLANFLVHSSNFGAILSSNTNVGSNKCNTATCATQRLANFLVHSSNFGAILSS TNVGSNTY-NH₂ (Daejeon, Republic of Korea)]. Ubiquitin was purchased from Sigma Aldrich (ubiquitin = MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLLFAGKQLEDGRTLS-DYNIQKESTLHLVLRLLRGG; St. Louis, MO, USA). Double-distilled H₂O (ddH₂O) was obtained from a Milli-Q Direct 16 system (Merck KGaA, Darmstadt, Germany). Irradiation with 1 sun was obtained with a Newport IQE-200 solar simulator (Irvine, CA, USA). ESI-MS and IM-MS analyses were performed by using a Waters Synapt G2-Si quadrupole time-of-flight ion mobility mass spectrometer equipped with an ESI source (DGIST Center for Core Research Facilities, Daegu, Republic of Korea). NMR studies of A β with **Ir-1** were conducted on a Bruker Avance 600 MHz spectrometer equipped with a TCI triple-resonance inverse detection cryoprobe. The data was processed by using TOPSPIN 2.1 (Bruker) software and assignments were made by using SPARKY 3.1134 software. Anaerobic reactions were performed in a N₂-filled glove box (Korea Kiyon, Bucheon-si, Gyeonggi-do, Republic of Korea). TEM images were taken by using a JEOL JEM-1400 transmission electron microscope (UNIST Central Research Facilities, Ulsan, Republic of Korea). Photophysical properties were measured by using an Agilent Cary 100 UV/Vis spectrophotometer and a Varian Cary Eclipse fluorescence spectrophotometer (UNIST Central Research Facilities, Ulsan, Republic of Korea). Timecorrelated single-photon counting (TCSPC) was performed for lifetime measurements with a Ti:sapphire laser Mira900 (Coherent, Santa Clara, CA, USA), monochromator Acton series SP-2150i (Princeton Instruments, Acton, MA, USA), and TCSPC module PicoHarp 300 (PicoQuant, Berlin,

Germany) together with MCP-PMT R3809U-59 (Hamamatsu, Shizuoka-ken, Japan) and fitted by PicoQuant FluoFit software (UNIST Central Research Facilities, Ulsan, Republic of Korea).

2.4.2. Synthesis of Ir-1

2-Phenylquinoline (680 mg, 3.3 mmol) was added to a solution of $\text{IrCl}_3 \cdot n\text{H}_2\text{O}$ (500 mg, 1.7 mmol) in a mixture of 2-methoxyethanol and H_2O (3:1). The solution was heated at reflux under N_2 (g) for 24 h. After cooling to room temperature, brown precipitates were obtained by treatment with additional H_2O . The crude product (cyclometalated chloride-bridged Ir(III) dimer, $[\text{Ir}(\text{C}^{\wedge}\text{N})_2(\mu\text{-Cl})_2]$) was washed with hexanes and cold diethyl ether several times, dried, and used without further purification.⁷³

A mixture of the cyclometalated chloride-bridged Ir(III) dimer (353 mg, 0.28 mmol), **1** (150 mg, 0.83 mmol), and Na_2CO_3 (294 mg, 2.8 mmol) was dissolved in 2-methoxyethanol. The mixture was heated at reflux under N_2 (g) for 12 h. After cooling to room temperature, the solution was concentrated, followed by the addition of H_2O . The organic phase was extracted with CH_2Cl_2 three times. The collected organic solution was dried with Na_2SO_4 and the solvent was removed under reduced pressure. The crude materials were purified by column chromatography (SiO_2 , 50:1 $\text{CH}_2\text{Cl}_2/\text{CH}_3\text{OH}$, $R_f = 0.6$) to give the product as a red powder (340 mg, 80%). FTIR (neat): $\nu = 3057, 2021, 1608, 1516, 1437, 1381, 1338, 1163, 1028, 762 \text{ cm}^{-1}$; UV/Vis (H_2O): $\lambda_{\text{max}} (\epsilon) = 463 \text{ nm} (5.78 (\pm 0.12) \times 10^3 \text{ M}^{-1} \text{ cm}^{-1})$. ^1H NMR (400 MHz, CDCl_3): $\delta = 8.79$ (d, $J = 8.0 \text{ Hz}$, 1H), 8.13 (t, $J = 8.0 \text{ Hz}$, 1H), 8.07 (m, 3H), 7.92 (dd, $J = 8.0 \text{ Hz}$, 1H), 7.80 (dd, $J = 8.0 \text{ Hz}$, 1H), 7.70 (dd, $J = 8.0 \text{ Hz}$, 1H), 7.67 (dd, $J = 8.0 \text{ Hz}$, 1H), 7.51 (m, 2H), 7.42 (d, $J = 8.0 \text{ Hz}$, 1H), 7.39 (ddd, 1H), 7.26 (ddd, 1H), 7.03 (m, 2H), 6.95 (m, 2H), 6.89 (dd, $J = 8.0 \text{ Hz}$, 1H), 6.72 (m, 1H), 6.60 (dt, $J = 6.8 \text{ Hz}$, 1H), 6.30 (m, 2H), 2.87 ppm (s, 6H); ^{13}C NMR (100 MHz, CDCl_3): $\delta = 173.0, 171.1, 169.2, 154.4, 151.8, 151.4, 148.7, 147.8, 147.0, 145.9, 145.1, 138.1, 136.3, 134.8, 129.4, 128.5, 126.0, 125.2, 121.5, 120.5, 116.1, 109.7, 108.8, 39.1 \text{ ppm}$; HRMS: m/z calcd for $\text{C}_{38}\text{H}_{29}\text{IrN}_4\text{NaO}_2 [\text{M} + \text{Na}]^+$: 789.1812; found: 789.1814; elemental analysis calcd (%) for $\text{C}_{38}\text{H}_{29}\text{IrN}_4\text{O}_2 \cdot 0.5\text{CH}_3\text{OH}$: C 59.14, H 4.00, N 7.17; found: C 59.00, H 4.01, N 7.19.

2.4.3. Photophysical Properties of Ir-1

Absorption and emission spectra were measured by UV-Vis and fluorescence spectrophotometers using a solution of **Ir-1** (20 μM in 20 mM HEPES, pH 7.4, 150 mM NaCl; final 1% v/v DMSO) at 298 K. Moreover, the quantum yield for phosphorescence (Φ_p) was calculated using $[\text{Ir}(\text{2-phenylquinoline})_2(2,2'\text{-bipyridine})](\text{PF}_6)$ ($\Phi_{\text{ref}} = 0.31$; 20 μM in 2-MeTHF solution) as a reference based on previously reported procedures.⁷⁴ The quantum yield of singlet oxygen ($^1\text{O}_2$) (Φ_s) was determined according to the method reported previously.⁷⁵ Solutions containing **Ir-1** (10 μM) and $^1\text{O}_2$ substrate [9,10-anthracenediyl-bi(methylene)dimalonic acid (ABDA, 100 μM)] were irradiated with 40% of 1 sun light. The absorbance of ABDA was obtained every 1 min up to 5 min. $[\text{Ru}(\text{bpy})_3]^{2+}$ was

2.4.4. Electrospray Ion Mobility Mass Spectrometry (ESI-IM-MS)

A β_{40} , α -Syn, hIAPP, and ubiquitin (100 μ M) were incubated with **Ir-1** or **1** (500 μ M) in 100 mM ammonium acetate (pH 7.5) at 37 $^{\circ}$ C without any agitation. Incubated peptides were diluted 10-fold and then injected into a mass spectrometer. The capillary voltage, sampling cone voltage, and source temperature were set to 2.8 kV, 70 V, and 40 $^{\circ}$ C, respectively. The backing pressure was adjusted to 3.2 mbar. Ion mobility wave height and velocity were adjusted to 10 V and 450 ms^{-1} , respectively, and gas flow for the helium cell and ion mobility cell was set to 120 and 30 mLmin^{-1} , respectively. Tandem MS (MS^2) analyses were additionally performed on the nonoxidized (Figure 2.14) and singly/doubly oxidized peptides. The ESI parameters and experimental conditions were same as those reported above. Collision-induced dissociation was conducted by applying the collision energy in the trap and adjusting LM resolution to 15. More than 200 spectra were obtained for each sample and averaged for analyses. To estimate collision cross-section values for obtained IM-MS data, calibration was also performed by following previously reported procedures (Figure 2.15).⁷⁷

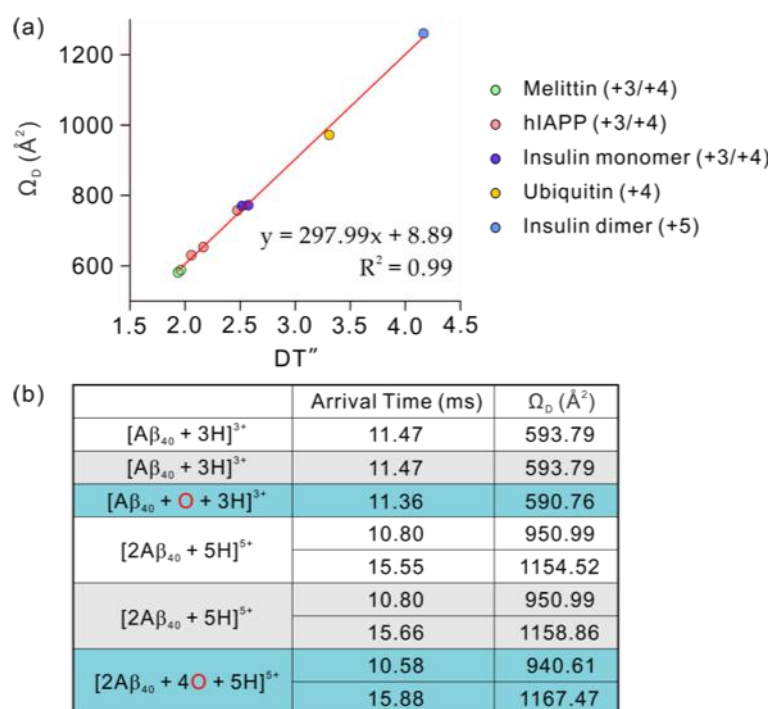


Figure 2.15. Calibration for the estimation of collision cross section values (Ω_D). Calibration was performed following the previously described procedure.⁷⁷ (a) Fitting plot to present a linear correlation between published collision cross section values of calibrant proteins and corrected drift time (DT''). All IM-MS results of calibrants were obtained in the same experimental parameters with those of A β_{40} . Published collision cross section values of calibrants could be found in previous reports.^{78–79} (b) Experimentally obtained cross section values for nonoxidized and oxidized A β_{40} . The IM-MS spectra for +5-charged dimers and +3-charged monomers are shown in Figures 2.4 and 2.6, respectively.

2.4.5. Mass Spectrometric Analyses

Oxidized A β ₄₀, α -Syn, hIAPP, and ubiquitin were observed upon incubation with **Ir-1** under aerobic conditions in the presence of light by using a Waters Synapt G2-Si Q-ToF mass spectrometer equipped with an ESI source. Only major charge states of all peptides (+3 for A β ₄₀ and hIAPP, +9 for α -Syn, and +5 for ubiquitin) were selected and shown in all mass spectra. Generally, exact mass should be calculated based on monoisotopic mass; however, in the present study, the oxidized peaks were assigned based on m/z values of the most abundant peaks because monoisotopic mass values of α -Syn could not be well resolved without a high-resolution mass spectrometer. For example, +3-charged A β ₄₀ was most dominantly found in ESI-MS (Figure 2.2a). Upon treatment of **Ir-1** and light, the singly oxidized A β ₄₀ ions were abundantly observed at 1449.6 m/z , corresponding to a 16 Da increase in mass from the nonoxidized A β ₄₀ peak at 1444.2 m/z (Figure 2.2a, bottom; blue). In the case of +9-charged α -Syn at 1607.8 m/z , the singly oxidized peak was not well defined due to overlap with sodiated ions at 1610.2 m/z . With the treatment of **Ir-1** and light, doubly oxidized α -Syn was found at 1611.3 m/z , which indicated an approximate 32 Da increase in mass (Figure 2.2b, bottom; blue). The +3-charged hIAPP presented an oxidized peak at 1306.9 m/z , indicating a 14 Da difference in mass from nonoxidized ions with 1302.2 m/z upon treatment with **Ir-1** and light (Figure 2.2c, bottom; blue). Different from A β ₄₀ and α -Syn, singly oxidized hIAPP indicated a 14 Da increase in mass. In the ESI-MS spectra of ubiquitin, the +5 charge state was most abundantly detected (Figure 2.7). Singly and doubly oxidized ubiquitin were found at 1717.2 and 1720.3 m/z , respectively, which were approximately 16 and 32 Da increases in mass from nonoxidized ubiquitin centered at 1713.9 m/z (Figure 2.7, bottom; blue).

2.4.6. Peptide Aggregation Experiments

Peptide aggregation experiments were conducted as previously published.⁸⁰ Amyloid- β (A β) or α -synuclein (α -Syn) was dissolved with ammonium hydroxide (NH₄OH, 1% v/v, aq), aliquoted, lyophilized, and stored at -80 °C. A stock solution (ca. 200 μ M) was prepared by re-dissolving A β or α -Syn with NH₄OH (1% w/v, aq, 10 μ L) followed by dilution with ddH₂O. In the case of hIAPP, the peptide was dissolved in 1,1,1,3,3,3-hexafluoro-2-propanol (HFIP, purchased from Tokyo Chemical Industries Inc., Ltd., Tokyo, Japan) at a concentration of 100 μ M to remove preformed aggregates. After the treatment with HFIP for 2 h at the room temperature, hIAPP aliquots were prepared by evaporating the solvent. The peptide concentration in solution was determined by measuring the absorbance of the solution at 280 nm (ϵ = 1450 M⁻¹cm⁻¹ for A β ₄₀; ϵ = 1490 M⁻¹cm⁻¹ for A β ₄₂; ϵ = 5400 M⁻¹cm⁻¹ for α -Syn; ϵ = 1280 M⁻¹cm⁻¹ for hIAPP).

For inhibition experiments, the peptide (25 μ M; 20 mM HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid), pH 7.4, 150 mM NaCl) was first treated with **Ir-1** or **1** (50 μ M; 1% v/v final DMSO concentration) followed by exposure to 1 sun light for 10 min. The resulting samples were

incubated at 37 °C for 24 h with constant agitation. For disaggregation experiments, the peptide was initially incubated at 37 °C for 24 h with steady agitation. **Ir-1** or **1** was added afterward followed by an additional 24 h of incubation at 37 °C with constant agitation. For the experiments under anaerobic conditions, all samples were prepared following the same procedure described above for aerobic samples in a N₂-filled glovebox.

2.4.7. 2D NMR Spectroscopy

2D band-selective optimized flip-angle short transient heteronuclear multiple quantum coherence (SOFAST-HMQC) NMR was applied to the sample containing uniformly-¹⁵N-labeled Aβ₄₀ and **Ir-1** at 10 °C.⁸¹ Uniformly-¹⁵N-labeled Aβ₄₀ (rPeptide, Bogart, GA, USA) was dissolved in 1% NH₄OH and lyophilized to ensure the absence of preformed aggregates. The peptide was re-dissolved in 3 mL of DMSO-*d*₆ (Cambridge Isotope, Tewksbury, MA, USA) and in buffer to a final peptide concentration of 80 μM (20 mM *d*₁₁-Tris, pH 7.4, 50 mM NaCl, 10% v/v D₂O). **Ir-1** was then titrated into the peptide solution from a 20 mM stock in DMSO-*d*₆. Following the completion of each titration (up to 2 equiv, 160 μM) the solution was exposed to ambient light within the NMR tube for 1 h and another spectrum was recorded. Each spectrum was obtained using 320 complex *t*₁ points and a 0.1 sec recycle delay on a Bruker Avance 600 MHz spectrometer. The data were processed using TOPSPIN 2.1 (Bruker) and assignment was performed using SPARKY 3.1134 using published assignments as a guide.^{82–84} Chemical shift perturbation (CSP) was calculated using the following equation:

$$\Delta\delta_{NH} = \sqrt{\Delta\delta_H^2 + \left(\frac{\Delta\delta_N}{5}\right)^2}$$

2.4.8. Gel Electrophoresis with Western Blotting (Gel/Western Blot)

The resultant Aβ species from both inhibition and disaggregation experiments were analyzed by gel electrophoresis followed by Western blotting (gel/Western blot) using an anti-Aβ antibody (6E10).⁸⁰ Each sample (10 μL; [Aβ₄₀ or Aβ₄₂] = 25 μM) was separated using a 10-20% gradient Tris-tricine gel (Invitrogen, Grand Island, NY, USA). The gel was transferred to a nitrocellulose membrane and blocked with a bovine serum albumin (BSA) solution (3% w/v; Sigma, St. Louis, MO, USA) in Tris-buffered saline (TBS; Fisher, Pittsburgh, PA, USA) containing 0.1% Tween-20 (TBS-T; Sigma-Aldrich) for 3 h at room temperature. The membrane was treated with the Aβ monoclonal antibody (6E10; Covance, Princeton, NJ, USA; 1:2,000; BSA, 2% w/v, in TBS-T) for overnight at 4 °C and then incubated with a horseradish peroxidase-conjugated goat anti-mouse secondary antibody (1:5,000; Cayman Chemical, Ann Arbor, MI, USA) in 2% BSA in TBS-T solution for 1 h at room temperature. Aβ species were visualized using the self-made ECL solution (2.5 mM luminol, 0.20 mM *p*-coumaric acid, and 0.018% H₂O₂ in 100 mM Tris, pH 8.6).

2.4.9. Transmission Electron Microscopy (TEM)

Peptide samples for TEM were prepared following the previously reported methods.⁸⁰ Glow discharged grids (Formvar/Carbon 300-mesh; Electron Microscopy Sciences, Hatfield, PA, USA) were treated with the resultant peptide (5 μ L) for 2 min at room temperature. Excess sample was removed with filter paper, and the grids were washed with ddH₂O three times. Each grid was stained with uranyl acetate (1% w/v ddH₂O; 5 μ L) for 1 min. Uranyl acetate was blotted off, and grids were dried for 20 min at room temperature. Images of samples were taken by a JEOL JEM-1400 transmission electron microscope (120 kV, 25,000 \times magnification).

2.5. Acknowledgments

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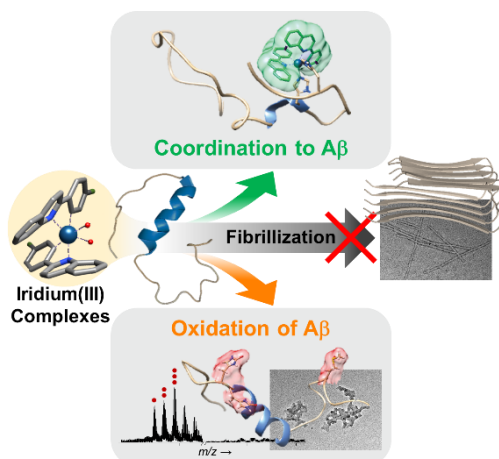
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Chapter 3.

Chemical Strategies to Modify Amyloidogenic Peptides by Iridium(III) Complexes: Coordination and Photo-induced Oxidation



The results and discussion presented in this chapter were described in the submitted manuscript [Kang, J.;[†] Nam, J. S.;[†] Lee, H. J.; Nam, G.; Rhee, H.-W.; Kwon, T.-H.; Lim, M. H. *Submitted* ([†]equal contribution)]. Professor Tae-Hyuk Kwon and Jung Seung Nam prepared Ir(III) complexes and measured their photophysical properties with data analysis. Dr. Hyuck Jin Lee and I performed the mass spectrometric investigations with data analysis. I carried out gel/Western blot, TEM, and cell studies with data analysis. I and Geewoo Nam wrote the manuscript under the direction of Professor Mi Hee Lim.

3.1. Introduction

A substantial amount of research efforts has been dedicated towards identifying the association of amyloidogenic peptides with the pathologies of neurodegenerative diseases. Among these amyloidogenic peptides, amyloid- β ($A\beta$), a proteolytic product of the amyloid precursor protein found in the AD-affected brain with a self-aggregation propensity, has been implicated as a pathological factor in Alzheimer's disease (AD).¹⁻⁴ As the main component of senile plaques, $A\beta$ accumulation is a major pathological feature of AD.^{1-3,5} Recent development in $A\beta$ research (e.g., clinical failures of $A\beta$ -directed therapeutics) has led to the re-evaluation of the amyloid cascade hypothesis.⁶ $A\beta$ pathology, however, remains a pertinent facet of the disease with indication of $A\beta$ oligomers as toxic species responsible for disrupting neuronal homeostasis.^{1-3,7} Furthering our elucidation of $A\beta$ pathology presents an investigative challenge arising from its heterogeneous nature and intrinsically disordered structure.^{1,2} To overcome this obstacle and advance our understanding of $A\beta$ -related contribution towards AD, in this study, we illustrate chemical approaches to modify $A\beta$ peptides at the molecular level using transition metal complexes.

Transition metal complexes are capable of harnessing a wide range of chemical and biological functionality, including peptide modifications (e.g., hydrolytic cleavage and peptide oxidation).⁸⁻³⁷ In particular, the ability of transition metal complexes to alter peptides stems from their properties, such as capacity for peptide coordination.^{17-29,36,37} Herein, we report effective chemical strategies for modifications of $A\beta$ peptides using a single Ir(III) complex in a photo-dependent manner (Figure 3.1). $A\beta$ modifications, achieved by our rationally engineered Ir(III) complexes, include two events: (i) complexation with $A\beta$ in the absence of light; (ii) $A\beta$ oxidation upon coordination and photoactivation, which can significantly regulate their aggregation and toxicity. Through our overall multidisciplinary studies, presented in this work, we demonstrate the feasibility of developing new chemical tactics for modifications of amyloidogenic peptides using transition metal complexes, useful for identifying their properties, such as aggregation, at the molecular level.

3.2. Results and Discussion

3.2.1. Rational Strategies for Peptide Modifications by Ir(III) Complexes

To chemically modify $A\beta$ peptides in a photo-irradiation-dependent manner (Figure 3.1a), four Ir(III) complexes (**Ir-Me**, **Ir-H**, **Ir-F**, and **Ir-F2**; Figure 3.1b) were rationally designed and prepared. Iridium is a third row transition metal exhibiting strong spin-orbit coupling at the center of Ir(III) complexes with facile electronic transitions.^{38,39} This spin-orbit coupling can be further strengthened by fine-tuning ancillary ligands of Ir(III) complexes. As a result, Ir(III) complexes confer notable photophysical properties upon excitation by relatively low energy irradiation in the visible range, including their ability

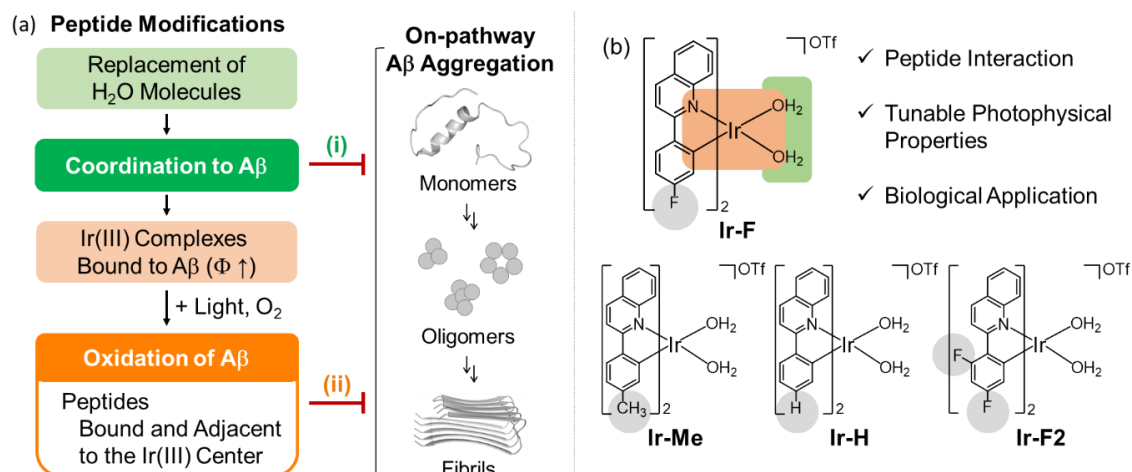
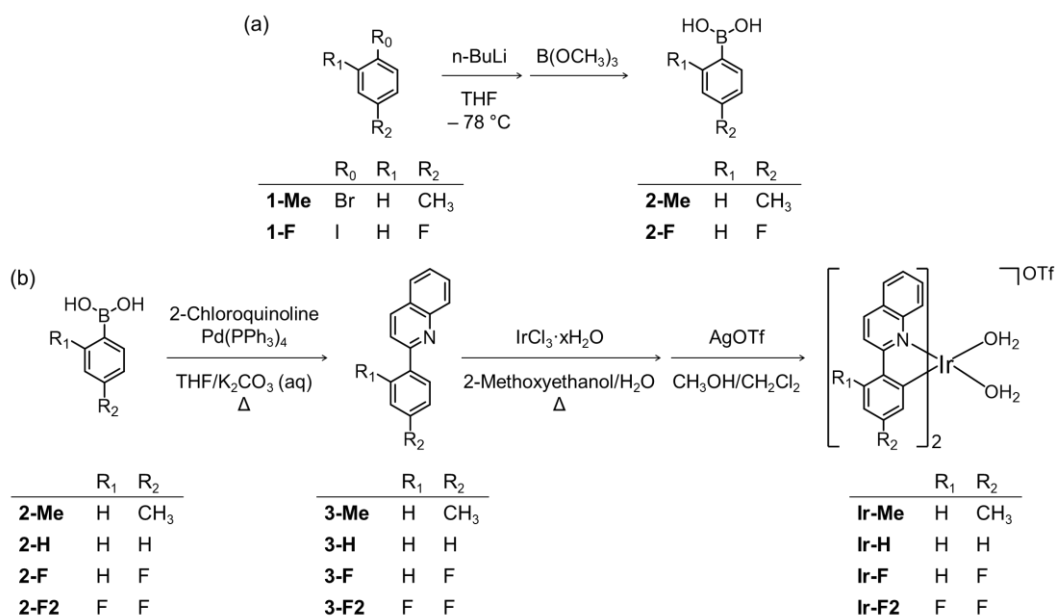


Figure 3.1. Chemical approaches to modify A β peptides using rationally designed Ir(III) complexes. (a) Two types of modifying A β peptides by Ir(III) complexes for control of A β aggregation: (i) coordination to A β peptides and (ii) oxidation of A β peptides mediated by coordination and photoactivation (Φ = emission quantum yield). (b) Design criteria and chemical structures of **Ir-F**, **Ir-Me**, **Ir-H**, and **Ir-F2**. Substituents are highlighted in gray.

Scheme 3.1. Synthetic routes to Ir(III) complexes.



to generate reactive oxygen species (ROS) via electron or energy transfer.^{38,40–42} Incorporation of 2-phenylquinoline derivatives as ligands yielded high emission quantum yield (Φ) and robust ROS generation.⁴⁰ Thereby, the ancillary ligands of four complexes were constructed based on the 2-phenylquinoline backbone by applying simple structural variations to provide appropriate structural and electronic environments to promote the photochemical activity of the corresponding Ir(III) complexes.⁴⁰ Moreover, fluorine atoms were introduced to the ancillary ligand framework, affording **Ir-F** and **Ir-F2**, to chemically impart the ability to interact with A β through hydrogen bonding, alter photophysical properties of the complexes, and enhance the molecules' biocompatibility.^{40,43–45} Two water (H₂O) molecules were incorporated as ligands to enable covalent coordination to A β via replacement with amino acid residues of the peptide, e.g., histidine (His).^{20,46,47} The four Ir(III) complexes were synthesized following the previously reported procedures with modifications (Scheme 3.1).^{20,48–50}

Table 3.1. Photophysical properties of Ir(III) complexes.

	Ir-Me		Ir-H		Ir-F		Ir-F2	
	– His	+ His	– His	+ His	– His	+ His	– His	+ His
$\lambda_{\text{ex, max}}$ (nm)	280 (\pm 27),	274 (\pm 29),	275 (\pm 29),	268 (\pm 32),	274 (\pm 34),	269 (\pm 33),	277 (\pm 36),	272 (\pm 37),
ϵ , $\times 10^3 \text{ M}^{-1}\text{cm}^{-1}$)	336 (\pm 14), 449 (\pm 3)	343 (\pm 16), 449 (\pm 3)	339 (\pm 15), 452 (\pm 3)	338 (\pm 15), 445 (\pm 3)	336 (\pm 17), 446 (\pm 4)	335 (\pm 16), 433 (\pm 4)	350 (\pm 21), 441 (\pm 7)	348 (\pm 19), 432 (\pm 6)
$\lambda_{\text{em, max}}$ (nm)	587	592	587	593	589	573	573	578
Φ	0.0038 (\pm 0.0007)	0.19 (\pm 0.01)	0.0037 (\pm 0.0006)	0.31 (\pm 0.03)	0.0071 (\pm 0.001)	0.26 (\pm 0.03)	0.0027 (\pm 0.0002)	0.081 (\pm 0.007)
τ (ns)	5.8 (\pm 1.8)	601 (\pm 20)	11 (\pm 1)	619 (\pm 61)	4.8 (\pm 1.9)	810 (\pm 23)	4.4 (\pm 0.4)	484 (\pm 41)
k_{r} ($\times 10^5 \text{ s}^{-1}$)	6.5	3.2	3.3	5.0	15	3.3	6.1	1.7
k_{nr} ($\times 10^5 \text{ s}^{-1}$)	1.7×10^3	13	883	11	2.6×10^3	9.1	2.3×10^3	19

3.2.2. Coordination-Dependent Photophysical Properties and Singlet Oxygen Production of Ir(III) Complexes

Photophysical properties of the prepared Ir(III) complexes were investigated by UV-Vis and fluorescence spectroscopy. Effects of His coordination to the Ir(III) center on Φ of Ir(III) complexes, a measure of the molecules' ability to produce singlet oxygen ($^1\text{O}_2$) with photoactivation, were comparatively evaluated. Upon addition of His, Φ of the Ir(III) complexes drastically increased (e.g., $\Phi_{\text{Ir-F}} = 0.0071$ versus $\Phi_{\text{Ir-F} + \text{His}} = 0.26$; Table 1), indicating His coordination of the complexes, which was further confirmed by electrospray ionization-mass spectrometry (ESI-MS) (Figure 3.2a). **Ir-F** showed the strongest binding affinity with His ($K_{\text{d}} = 2.7 \times 10^{-6} \text{ M}$; Figure 3.2b) and generated the largest amount of $^1\text{O}_2$ upon photoactivation among four Ir(III) complexes (Figure 3.3). Based on these

amount of $^1\text{O}_2$ upon photoactivation among four Ir(III) complexes (Figure 3.3). Based on these properties, we selected **Ir-F** as a representative candidate of our Ir(III) complexes and illustrated its ability to modify A β peptides in detail (vide infra).

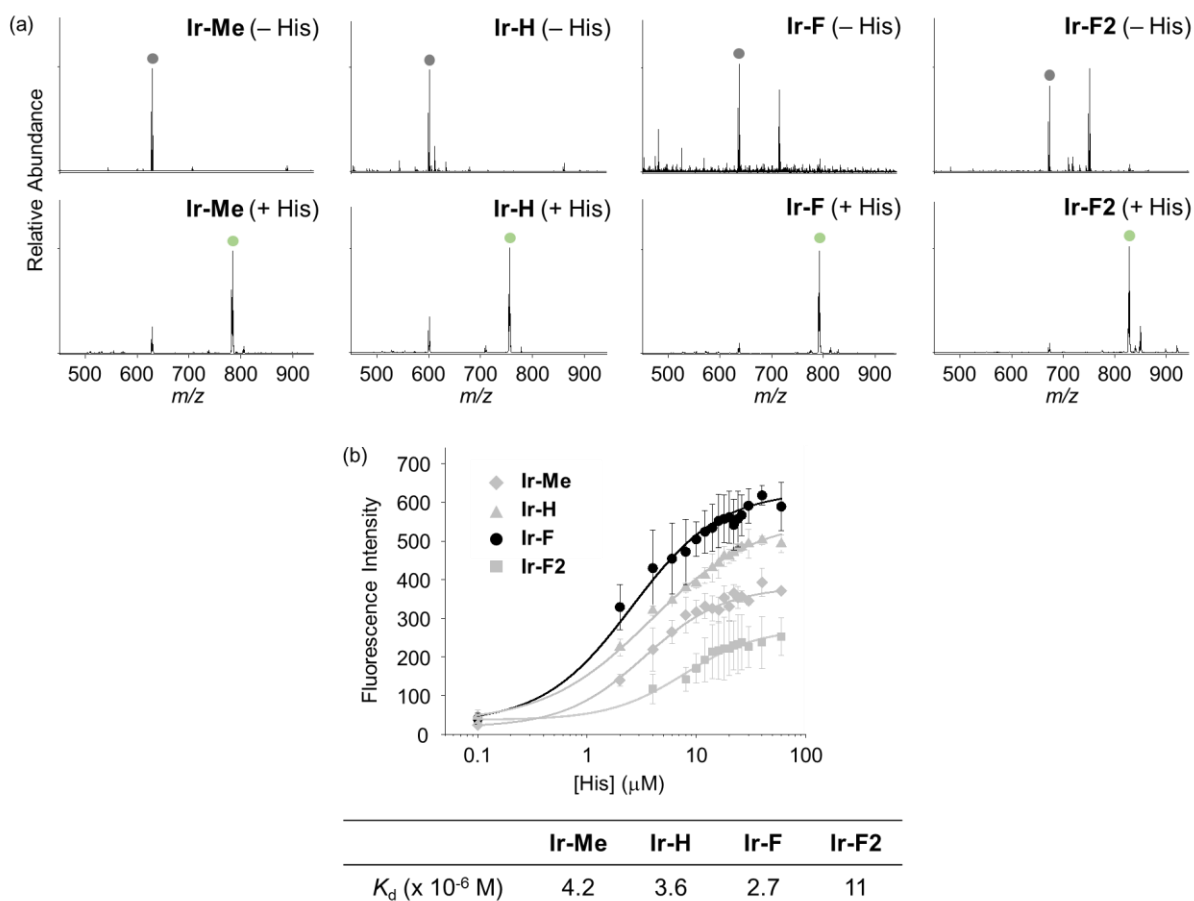


Figure 3.2. Histidine binding of Ir(III) complexes. (a) ESI-MS analysis of Ir(III) complexes (gray dots; top) with and without His. The complex formation between His and Ir(III) complexes that do not contain two H_2O molecules on the Ir(III) center [Ir(III) complexes - $2\text{H}_2\text{O}$] was observed (light green dots; bottom). Conditions: [Ir(III) complex] = 20 μM ; [His] = 200 μM ; room temperature; 2 h; no agitation. (b) His binding affinities of Ir(III) complexes. Dissociation constants (K_d) were determined through His titration experiments. Conditions: [Ir(III) complex] = 2 μM ; [His] = 0-60 μM ; room temperature; 2 h; no agitation.

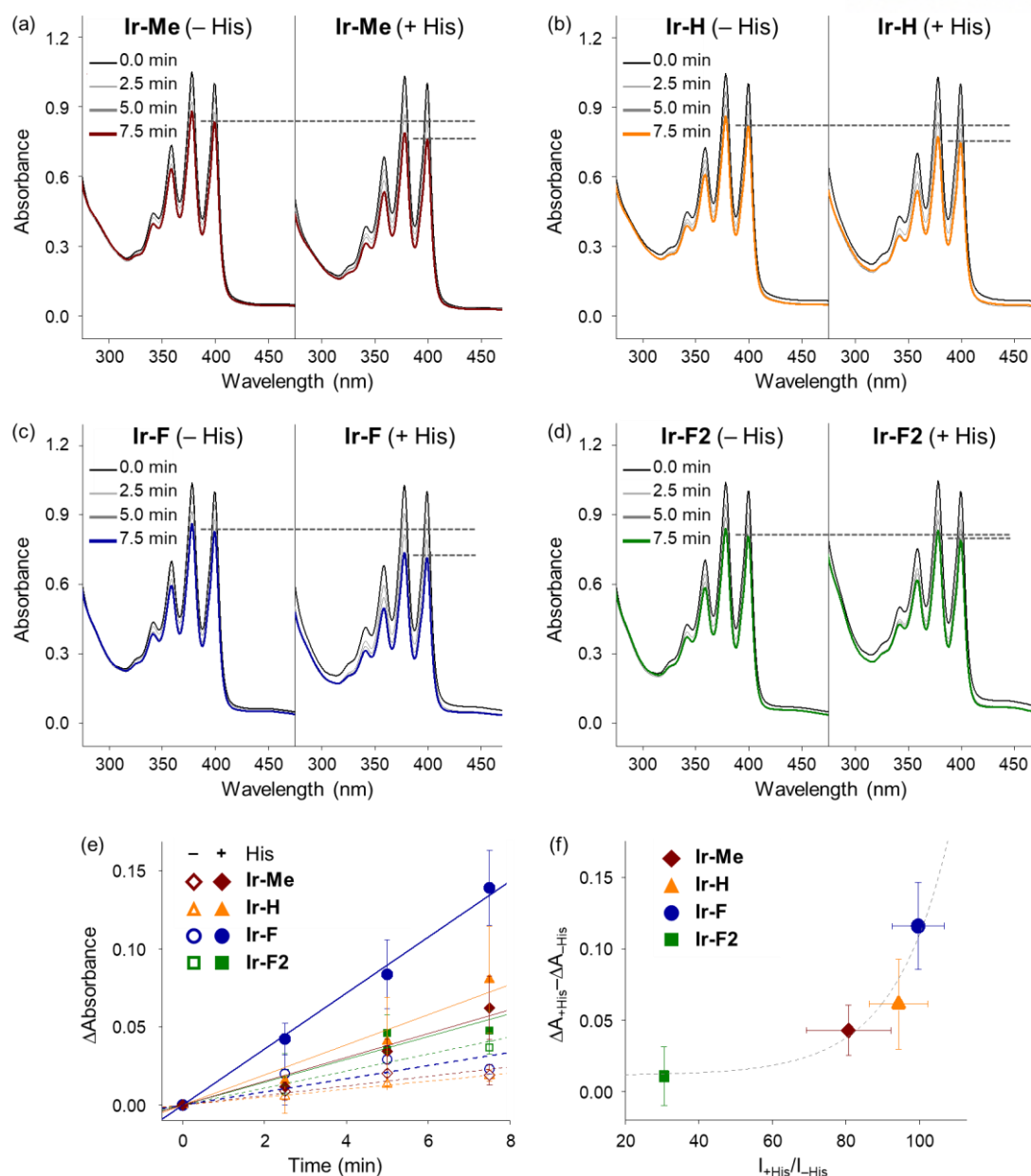


Figure 3.3. Analysis of the amount of singlet oxygen ($^1\text{O}_2$) generated by Ir(III) complexes in the absence and presence of histidine. (a-d) Time-dependent absorbance of 9,10-anthracenediyl-bis(methylene)dimalonic acid (ABDA) upon $^1\text{O}_2$ generation triggered by (a) **Ir-Me**, (b) **Ir-H**, (c) **Ir-F**, and (d) **Ir-F2**. (e) Absorbance attenuation of ABDA with photoactivated Ir(III) complexes. (f) Correlation between the ability to produce $^1\text{O}_2$ and the emission intensity of Ir(III) complexes upon His binding. Note that $^1\text{O}_2$ generation is closely related to the triplet-to-singlet electronic transition of the complexes. Since $^1\text{O}_2$ generation takes place through energy transfer, it is important that the energy donor (i.e., Ir(III) complex) can efficiently emit the photon (phosphorescence) by transferring its energy to the energy acceptor (ground state O_2). Conditions: [Ir(III) complex] = 10 μM ; [His] = 0 or 10 μM ; [ABDA] = 100 μM ; room temperature; 40% of 1 sun light.

3.2.3. Photoirradiation-Dependent Peptide Modifications by Ir(III) Complexes

Modifications of A β peptides upon treatment with **Ir-F** were monitored via mass spectrometric techniques [i.e., ESI-MS, ESI-MS², and ion mobility-mass spectrometry (IM-MS)]. The ESI-MS analysis of **Ir-F**-treated A β samples revealed the complex formation between A β and **Ir-F'** (the **Ir-F** form that does not contain the two H₂O ligands; Figure 3.4b) in the absence of light as an indication at 1653 m/z (Figure 3.4a, middle; green). To identify the molecular species corresponding to 1653 m/z , the peak was further analyzed via ESI-MS² in conjunction with collision-induced dissociation (CID; Figure 3.4c). The detected ion fragments exhibited m/z values responsible for A β ₄₀ and **Ir-F'**. Therefore, our MS results demonstrate the complexation between A β and **Ir-F** with loss of two H₂O molecules from the Ir(III) center (Figure 3.1b). Note that the m/z value of the **Ir-F'**–A β ₄₀ complex is equal to that of [A β ₄₀ + 4OTf + 2H₂O]; thus, we cannot rule out the co-existence of the complex and an OTf adduct.

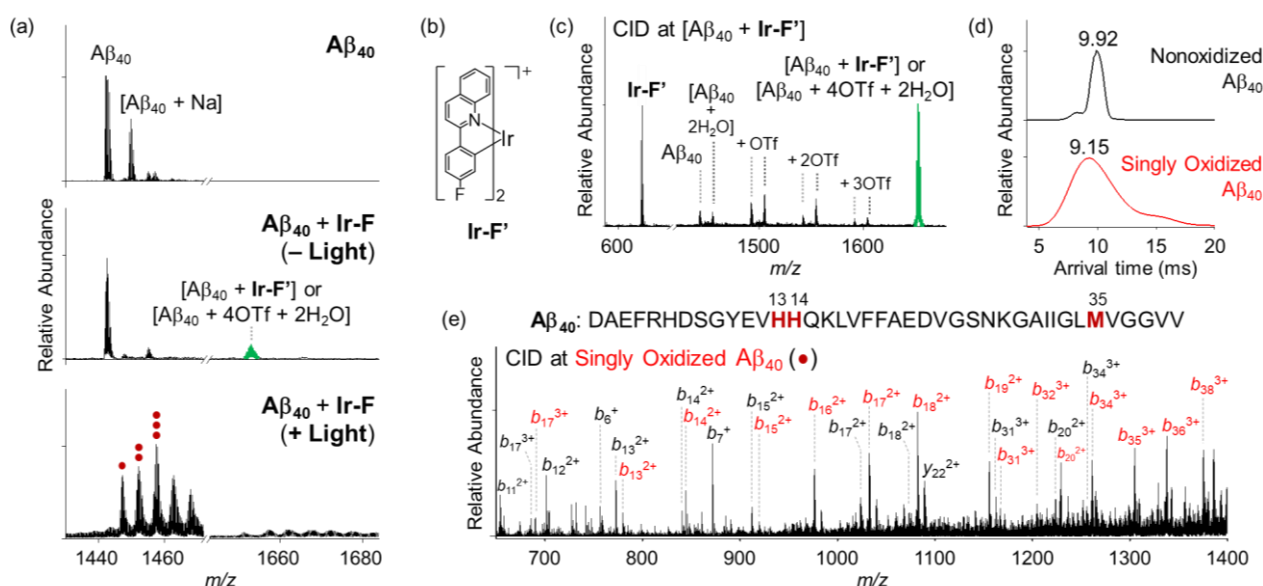


Figure 3.4. Analysis of the A β ₄₀ species generated upon treatment with **Ir-F**. (a) ESI-MS spectra of **Ir-F**-incubated +3-charged A β ₄₀ with and without light. The peak indicated in green corresponds to a complex of A β ₄₀ and **Ir-F'** [structure shown in (b)]. The peaks corresponding to oxidized A β ₄₀ species are indicated with red dots. The number of red dots presents the number of oxygen atoms incorporated into A β ₄₀. (c) Collision-induced dissociation (CID) spectrum at 1653 m/z [green peak from (a)]. (d) Arrival time distributions (ATDs) between nonoxidized and singly oxidized A β ₄₀ monomers. (e) Sequence of A β ₄₀ and CID spectrum of the singly oxidized A β ₄₀ found in (a). Monooxidized b fragments are notated in red. Charges are omitted in the MS spectra. Conditions: [A β ₄₀] = 100 μ M; [**Ir-F**] = 500 μ M; 37 $^{\circ}$ C; 1 h; no agitation; 1 sun light for 10 min (for the samples treated with light); aerobic conditions.

Upon photoirradiation, the ESI-MS analysis of **Ir-F**-treated $A\beta_{40}$ samples led to the detection of oxidized $A\beta_{40}$ (Figure 3.4a, bottom). $A\beta_{40}$ oxidation manifested a conformational change as probed by IM-MS (Figure 3.4d). The most dominant arrival time distribution (ATD) of the singly oxidized $A\beta_{40}$ treated with **Ir-F** showed a broad peak at 9.15 ms, while that of native $A\beta_{40}$ indicated a peak at 9.92 ms. These results suggest that $A\beta_{40}$ oxidation induced by **Ir-F** can alter the structural distribution of $A\beta_{40}$. Similar observations were observed with **Ir-Me**, **Ir-H**, and **Ir-F2**, where the complexes were able to oxidize $A\beta_{40}$ and consequently vary its structural distribution (Figures 3.5 and 3.6). In order to determine the location of peptide oxidation, the $A\beta$ fragment ions, generated by selectively applying collisional energy to singly oxidized $A\beta$, were analyzed by ESI-MS² (Figure 3.4e). All b fragments smaller than b_{13} were detected in their nonoxidized forms, while those larger than b_{34} were only

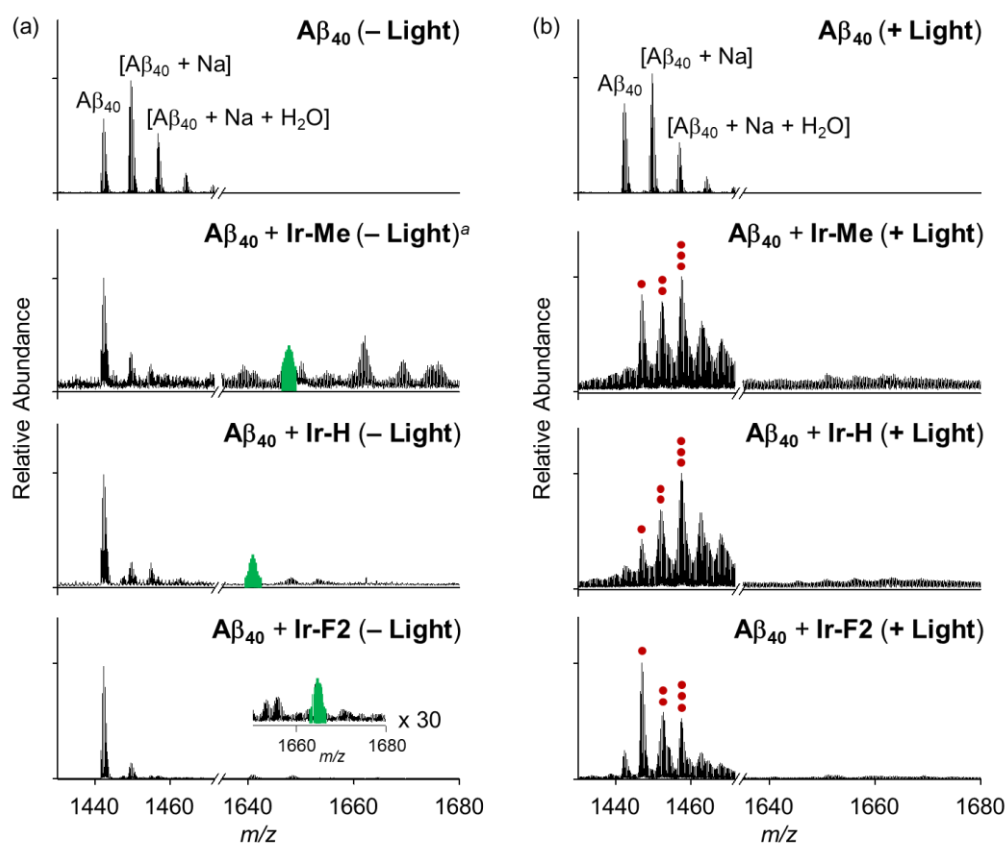


Figure 3.5. ESI-MS spectra of +3-charged $A\beta_{40}$ treated with **Ir-Me**, **Ir-H**, and **Ir-F2** in the (a) absence and (b) presence of light. The peaks [shown in (a)] corresponding to the complexes composed of $A\beta_{40}$ and Ir(III) complexes are indicated in green. The peaks [shown in (b)] corresponding to oxidized $A\beta_{40}$ species are highlighted with red dots. The number of red dots presents the number of oxygen atoms incorporated into $A\beta_{40}$. Conditions: $[A\beta_{40}] = 100 \mu\text{M}$; $[\text{Ir(III) complex}] = 500 \mu\text{M}$; 37°C ; 1 h (^a0.5 h for the sample of $A\beta_{40}$ with **Ir-Me** without light treatment); no agitation; 1 sun light for 10 min (for the samples treated with light); aerobic conditions.

monitored in their oxidized forms. The *b* fragments between b_{13} and b_{34} were indicated in both their oxidized and nonoxidized forms. Such observations, along with previous reports regarding A β oxidation,^{19,51} suggest His13, His14, and Met35 of A β as plausible oxidation sites. Collectively, our studies demonstrate that A β peptides can be modified upon treatment with **Ir-F** [(i) coordination to A β by replacing two H₂O ligands with the peptide in the absence of light; (ii) coordination-mediated oxidation of A β at three possible amino acid residues (e.g., His13, His14, and Met35) upon photoactivation (Figure 3.1a)].

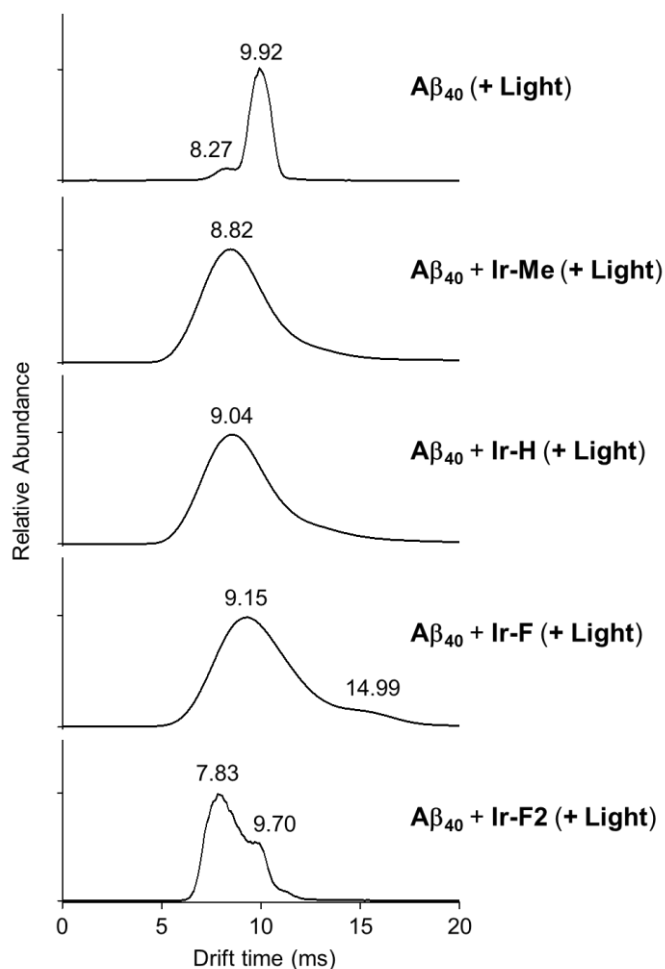


Figure 3.6. IM-MS spectra of +3-charged A β_{40} incubated with and without Ir(III) complexes. Arrival time distributions (ATDs) for nonoxidized (top; the “A β_{40} + Light” sample) and singly oxidized A β_{40} generated upon treatment of light-activated Ir(III) complexes were detected.

3.2.4. Effects of Peptide Modifications Triggered by Ir(III) Complexes on A β Aggregation

Based on the photoirradiation-dependent A β modifications by Ir(III) complexes, the impact of such peptide variations on the aggregation pathways of A β was determined employing A β_{40} and A β_{42} , two main A β isoforms found in the AD-affected brain.^{1-4,52-56} For these experiments, freshly prepared A β solutions were treated with Ir(III) complexes with and without light under both aerobic and anaerobic conditions. The molecular weight (MW) distribution and the aggregate morphology of resultant A β species were analyzed by gel electrophoresis with Western blotting (gel/Western blot) using an anti-A β antibody (6E10) and transmission electron microscopy (TEM), respectively (Figure 3.7a).

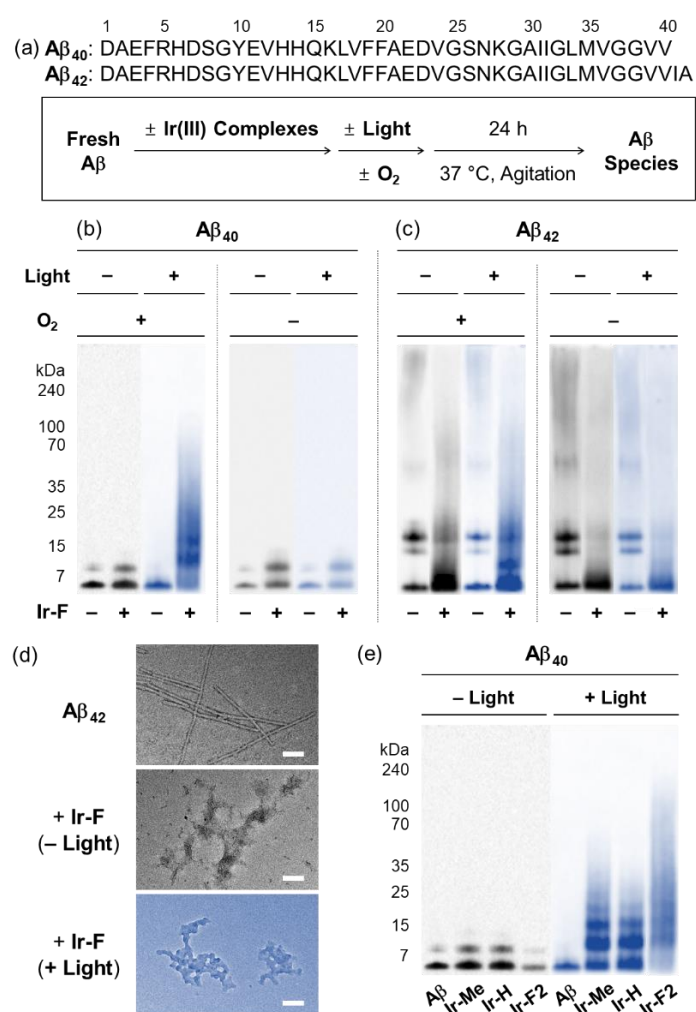


Figure 3.7. Change in the formation of A β aggregate with incubation of Ir(III) complexes. (a) Sequences of A β_{40} and A β_{42} and Scheme of the inhibition experiments. (b,c,e) Analysis of the resultant A β_{40} and A β_{42} species generated under various conditions by gel/Western blot with an anti-A β antibody (6E10). (d) TEM images of the A β aggregates formed from (c) (scale bar = 100 nm). Conditions: [A β] = 25 μ M; [Ir(III) complexes] = 250 μ M; 37 $^\circ$ C; 24 h; constant agitation; 1 sun light for 10 min (for the samples treated with light).

Under aerobic conditions (Figure 3.7b, left), the aggregation of A β ₄₀ was affected with treatment of **Ir-F** prompting a shift in the MW distributions in the absence of light. Photoactivation of the **Ir-F**-treated A β ₄₀ sample resulted in a more diverse MW distribution compared to that of the corresponding sample without light (light, MW \leq 100 kDa; no light, MW < 15 kDa). The distinct modulation of A β ₄₀ aggregation upon addition of **Ir-F** with photoirradiation is likely a consequence of the complex's ability to generate ¹O₂ and oxidize A β through photoactivation as observed in our spectrometric studies (vide supra; Figure 3.4). Therefore, the same experiments were performed under anaerobic conditions to

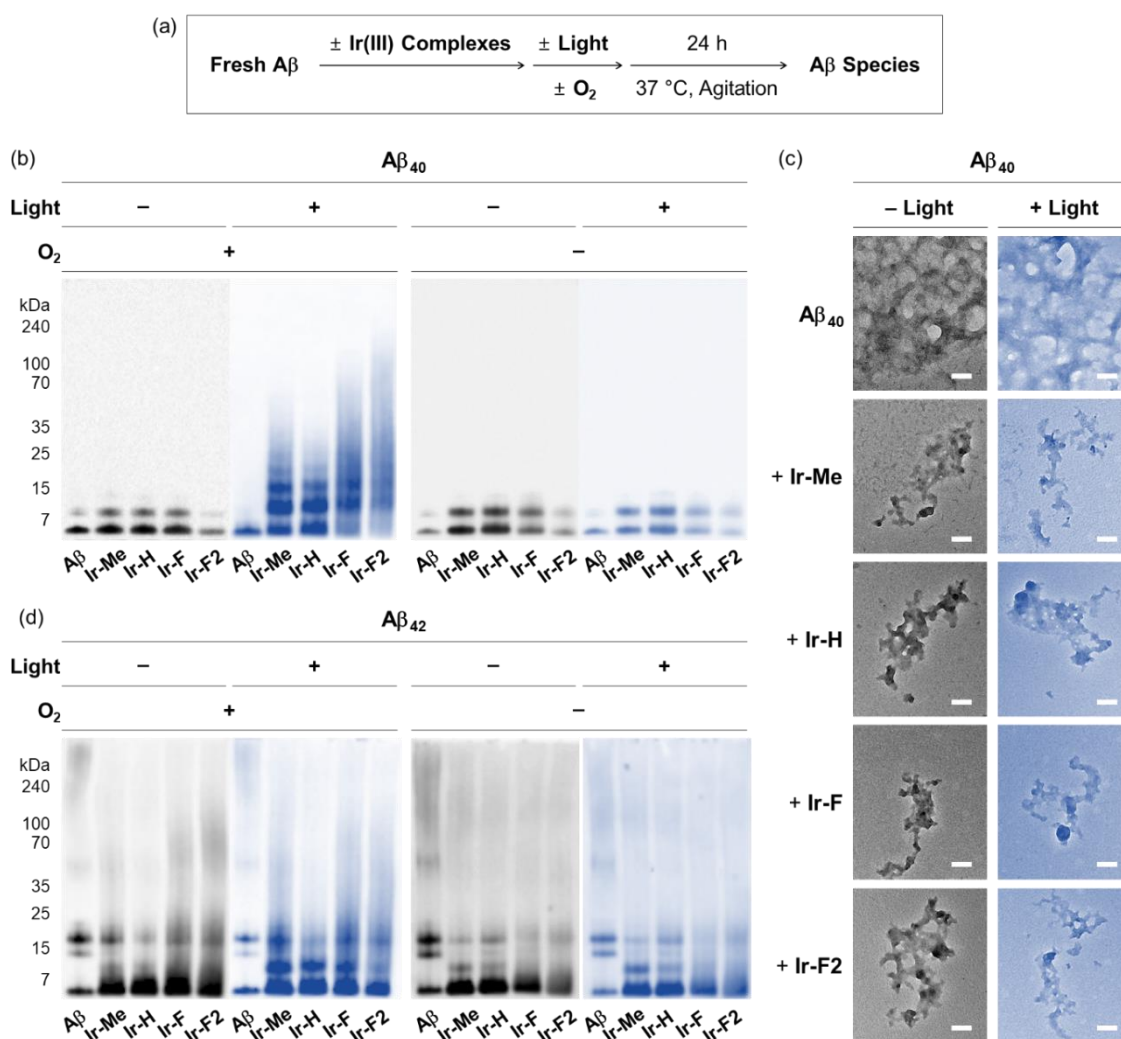


Figure 3.8. Influence of Ir(III) complexes on the formation of A β aggregates. (a) Scheme of the experiments. Analyses of the resultant (b) A β ₄₀ and (d) A β ₄₂ species produced from various experimental conditions by gel/Western blot with an anti-A β antibody (6E10). Conditions: [A β] = 25 μ M; [Ir(III) complex] = 250 μ M; 1 sun light for 10 min (for the samples treated with light). (c) TEM images of the A β ₄₀ aggregates produced from (b) (scale bar = 100 nm).

directly monitor the role of O₂ in **Ir-F**'s modulative reactivity against A β ₄₀ aggregation. In the absence of O₂ (Figure 3.7b, right), A β ₄₀ aggregation was also altered by **Ir-F** regardless of light treatment. Our results suggest that both light and O₂ are important in the regulation of A β ₄₀ aggregation through coordination-/photo-mediated peptide oxidation triggered by **Ir-F**. In addition, in the absence of light and O₂, A β ₄₀ aggregation is directed by the covalent interactions between **Ir-F** and the peptide. Similar modulation of A β ₄₂ aggregation was observed upon incubation with **Ir-F** exhibiting different MW distributions compared to the A β ₄₂ samples without **Ir-F** in the absence and presence of light and O₂ (Figure 3.7c). Moreover, smaller amorphous aggregates of both A β ₄₀ and A β ₄₂, reported to be less toxic,^{57,58} were visualized by TEM from the samples containing **Ir-F** regardless of irradiation (Figures 3.7d and 3.8c).

Furthermore, preformed A β aggregates, generated at various preincubation time points (i.e., 2, 4, and 24 h), were disassembled and their aggregation pathways were altered, when **Ir-F** was introduced (Figure 3.9). Such **Ir-F**-induced effects on preformed A β aggregates were observed to be dependent on photoirradiation. Moreover, the aggregation of both A β ₄₀ and A β ₄₂ was also changed with addition of the other Ir(III) complexes (i.e., **Ir-Me**, **Ir-H**, and **Ir-F2**) with and without light (Figures 3.7e, 3.8 and 3.9).

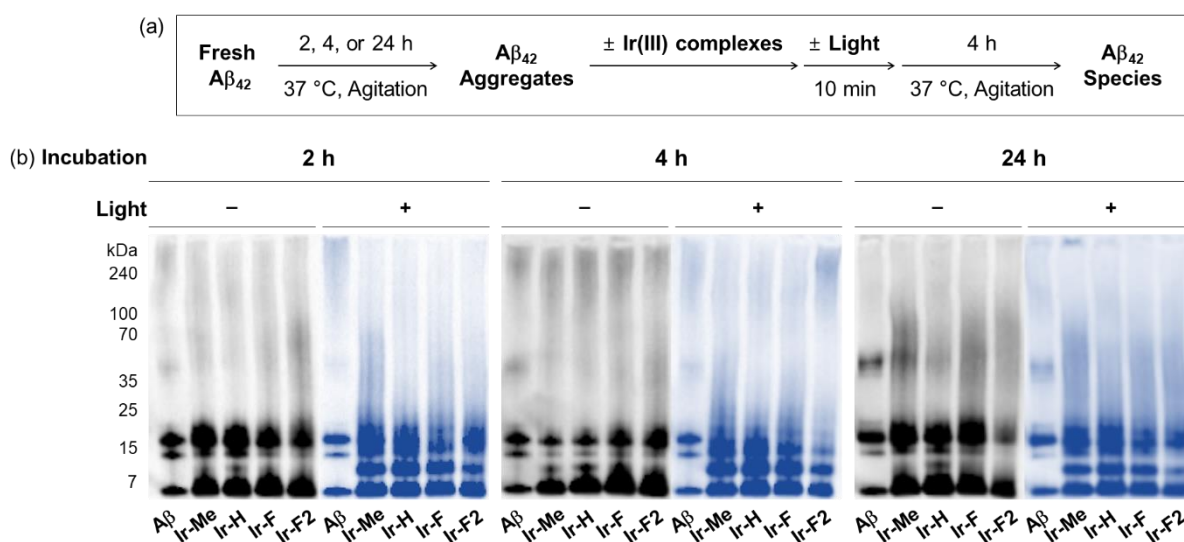


Figure 3.9. Impact of Ir(III) complexes on the disassembly of preformed A β ₄₂ aggregates produced at various incubation time points (i.e., 2 h, 4 h, and 24 h). (a) Scheme of the experiments. (b) Analysis of the resultant A β ₄₂ species by gel/Western blot with an anti-A β antibody (6E10). Conditions: [A β ₄₂] = 25 μ M; [Ir(III) complex] = 250 μ M; 1 sun light for 10 min (for the samples treated with light).

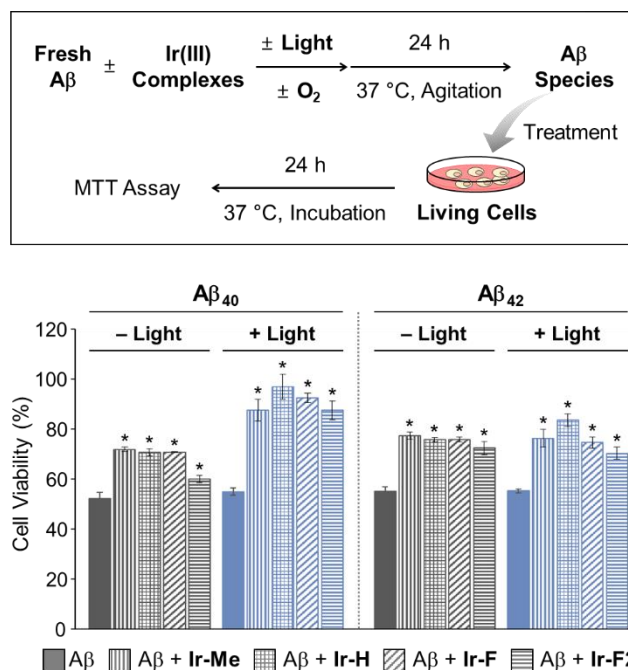


Figure 3.10. Viability of N2a cells upon 24 h treatment with Aβ species produced by incubation with Ir(III) complexes for 24 h with and without light activation. Cell viability (%), measured by the MTT assay, was calculated compared with that treated with an equivalent amount of DMSO only. Conditions (final concentration): [Aβ] = 20 μM; [Ir(III) complexes] = 5 μM. Error bars represent the standard error of the mean from three independent experiments. **P* < 0.05.

3.2.5. Cytotoxicity of Aβ Species Generated upon Incubation with Ir(III) Complexes

Moving forward, the toxicity of Aβ species produced with treatment of our Ir(III) complexes was determined in murine Neuro-2a (N2a) neuroblastoma cells by the MTT assay [MTT = 3-(4,5-dimethyl-2-thiazolyl)-2,5-diphenyl-2*H*-tetrazolium bromide] (Figure 3.10). The cytotoxicity of Aβ₄₀ species incubated with our Ir(III) complexes was noticeably reduced in a photoirradiation-dependent manner. In the absence of light, the Aβ₄₀ samples incubated with our Ir(III) complexes exhibited a decrease in cytotoxicity (ca. 20%) than the sample of the complex-free Aβ₄₀. As for the photoirradiated samples, Aβ₄₀-induced toxicity was lowered by ca. 35% when being treated with our Ir(III) complexes. Furthermore, the cytotoxicity of Aβ₄₂ species formed with Ir(III) complexes was also diminished by ca. 20% regardless of photoactivation. Note that the survival (≥ 80%) of cells added with our Ir(III) complexes under the concentration used for cell studies with Aβ peptides was observed with and without light exposure (Figure 3.11).

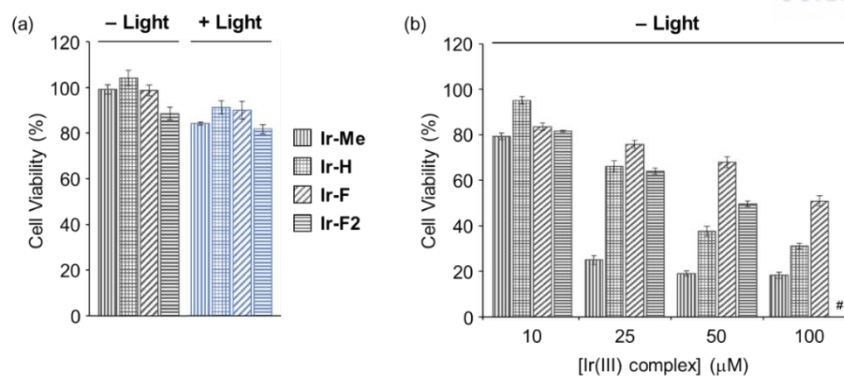


Figure 3.11. Viability of N2a cells with Ir(III) complexes. (a) Cell viability of Ir(III) complexes (5 μM) in the absence and presence of light. (b) Survival of the cells treated with different concentrations of Ir(III) complexes (10-100 μM; #the value was not obtained due to limited solubility) in the absence of light exposure. Cell viability (%), measured by the MTT assay, was calculated compared with cells obtained with an equivalent amount of DMSO only. Error bars represent S.E.M. from three independent experiments.

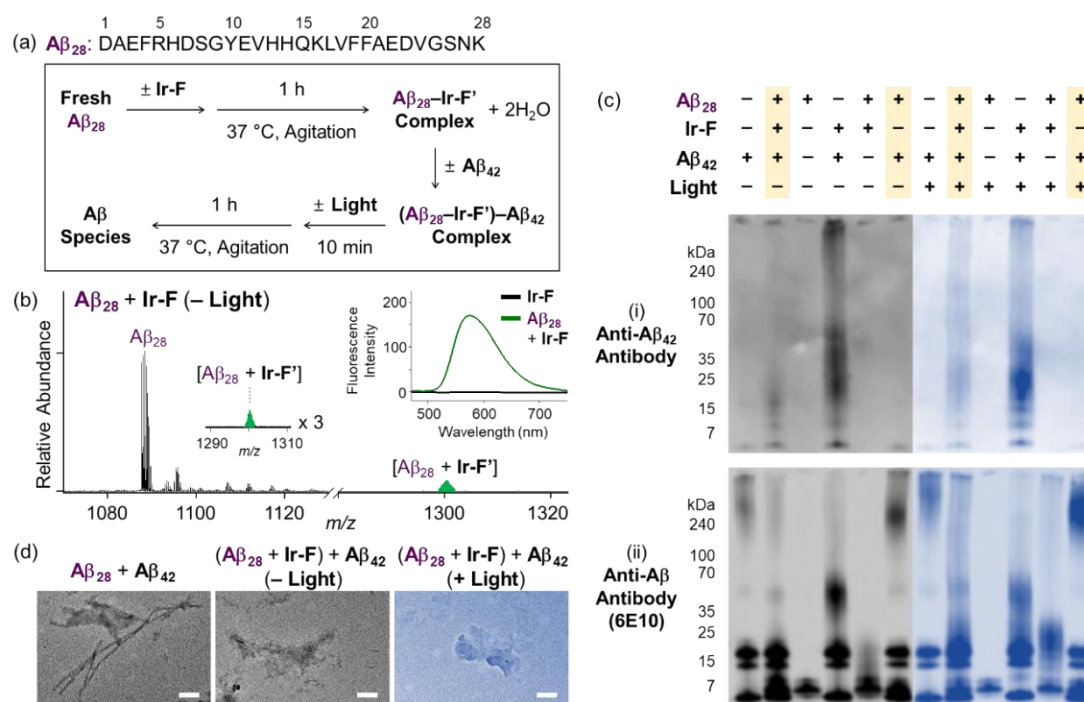


Figure 3.12. Impact of Ir-F-preincubated Aβ₂₈ on the aggregation of Aβ₄₂. (a) Sequence of Aβ₂₈ and scheme of the experiments. (b) ESI-MS spectrum of +3-charged Aβ₂₈ upon incubation with Ir-F. The complex peak is indicated in green. (Inset) Fluorescence response of Ir-F to Aβ₂₈ (λ_{ex} = 433 nm). Charges are omitted in the MS spectra. Conditions: [Aβ₂₈] = 100 μM; [Ir-F] = 100 μM; 37 °C; 1 h; no agitation; 1 sun light for 10 min (for the samples treated with light); aerobic conditions. (c) Analysis of the resultant Aβ species, obtained by addition of Aβ₄₂ into Ir-F preincubated with Aβ₂₈, by gel/Western blot with (i) anti-Aβ₄₂ and (ii) anti-Aβ (6E10) antibodies. (d) TEM images of the Aβ aggregates produced from (c) (scale bar = 100 nm). Conditions: [Aβ₂₈] = 50 μM; [Ir-F] = 10 μM; [Aβ₄₂] = 20 μM; 37 °C; 2 h; constant agitation; 1 sun light for 10 min (for the samples treated with light); aerobic conditions.

3.2.6. Ternary Complexation with A β and Intramolecular and Intermolecular A β Oxidation

Premised on **Ir-F**'s covalent bond formation with A β and oxidation of A β (vide supra), additional studies regarding ternary complexation and promotion of intermolecular oxidation of A β were carried out employing **Ir-F** (Figure 3.12). A β_{28} , a fragment of A β equipped with the metal binding and self-recognition sites of A β_{40} and A β_{42} with a relatively less propensity to aggregate than the full-length peptide,^{1,59–61} was used to form a complex with **Ir-F**' (Figure 3.4b) as evidenced by ESI-MS (1301 m/z ; Figure 3.12b) and increased fluorescence (Figure 3.12b, inset). As shown in Figure 3.12a, following incubation, the sample of the A β_{28} –**Ir-F**' complex was treated to freshly prepared A β_{42} to monitor its effect on A β_{42} aggregation. Based on the gel/Western blot and TEM analyses, the aggregation of A β_{42} was modulated by the A β_{28} –**Ir-F**' complex (Figure 3.12c and d). Our mass spectrometric studies confirmed that such control of A β_{42} aggregation by the A β_{28} –**Ir-F**' complex was a result of the ternary complex formation with A β_{42} , i.e., (A β_{28} –**Ir-F**')–A β_{42} , and (ii) oxidation of A β_{42} , both intramolecular and intermolecular, upon photoactivation (Figure 3.13). Based on previous reports detailing intermolecular interactions between A β peptides, hydrophobic interactions between the self-recognition site (LVFFA) of A β are likely responsible for ternary complexation,^{1,2,62} consequentially altering the

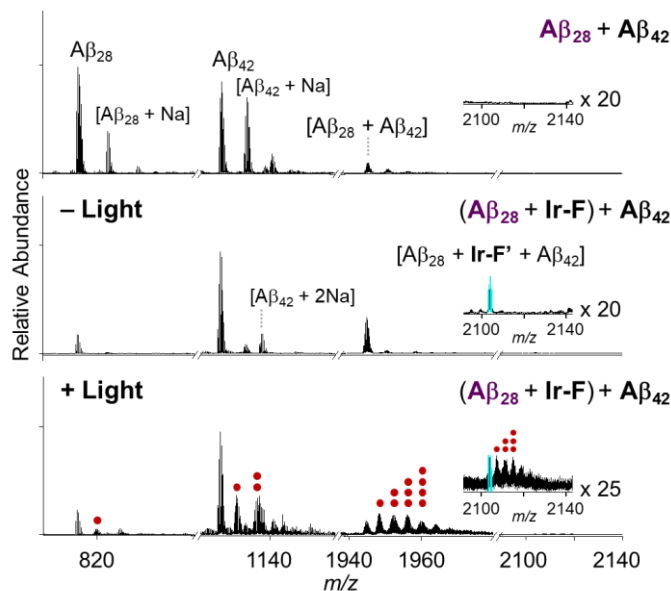


Figure 3.13. ESI-MS spectra of **Ir-F**-incubated +4-charged A β_{28} and A β_{42} with and without light. The peak indicated in cyan refers to a ternary complex of A β_{28} , **Ir-F**', and A β_{42} . The peaks corresponding to oxidized peptides (i.e., A β_{28} , A β_{42} , and A β_{28} with A β_{42}) are indicated with red dots. The number of red dots presents the number of oxygen atoms incorporated into each peptide. Charges are omitted in the MS spectra. Conditions: [A β_{28}] = 100 μ M; [**Ir-F**] = 100 μ M; [A β_{42}] = 100 μ M; 37 $^{\circ}$ C; 2 h; no agitation; 1 sun light for 10 min (for the samples treated with light); aerobic conditions.

aggregation pathways of A β in the absence of photoirradiation. Furthermore, these studies indicate that intermolecular oxidation of A β can be promoted by **Ir-F** upon photoactivation (Figures 3.13 and 3.14). This observation may explain the distinct difference between the modulation of A β aggregation with and without light as the intermolecular A β oxidation by Ir(III) complexes could modify A β at sub-stoichiometric levels.

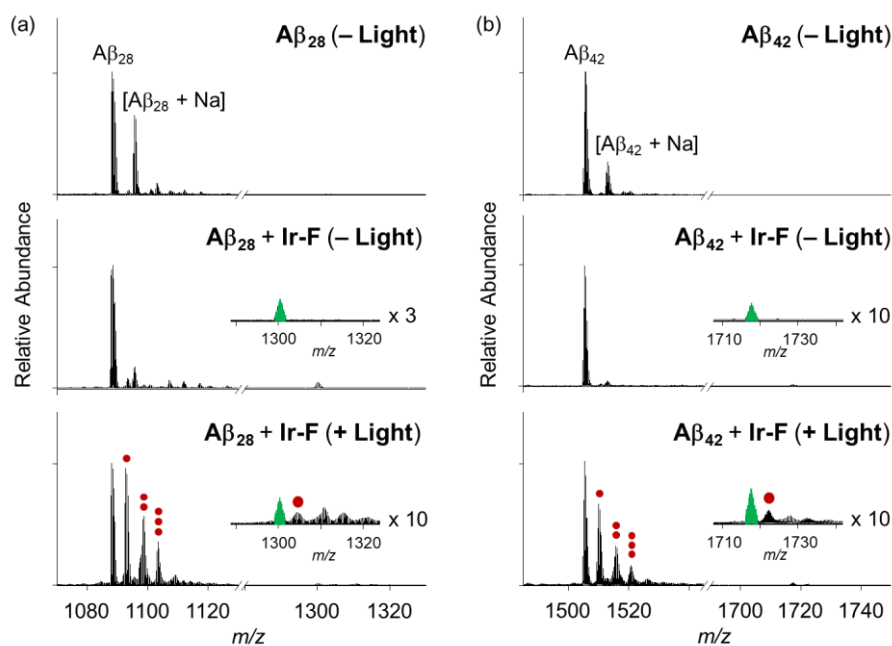


Figure 3.14. ESI-MS spectra of +3-charged (a) A β_{28} or (b) A β_{42} treated with **Ir-F** in the absence and presence of light. The peak indicated in green refers to the complex generation between A β and **Ir-F'** (the **Ir-F** form that does not contain two H₂O molecules). The peaks corresponding to oxidized A β species are indicated with red dots. The number of red dots presents the number of oxygen atoms incorporated into A β . Conditions: [A β] = 100 μ M; [Ir-F] = 100 μ M; 37 $^{\circ}$ C; 1 h; no agitation; 1 sun light for 10 min (for the samples treated with light); aerobic conditions.

3.3. Conclusions

Effective chemical strategies (i.e., coordination to A β and coordination-/photo-mediated A β oxidation) for modifications of A β peptides using a single Ir(III) complex were rationally developed. Such changes in A β peptides are able to lead to the noticeable modulation of their aggregation and toxicity in living cells. Our Ir(III) complexes can covalently bind to A β by replacing two H₂O ligands with A β regardless of light and O₂ [coordination to A β ; Figure 3.1a (i)]. In the presence of light and O₂, Ir(III) complexes bound to A β are capable of inducing the intramolecular and intermolecular oxidation of A β at His13, His14, and/or Met35 [oxidation of A β ; Figure 3.1b (ii)]. Taken together, our multidisciplinary studies

demonstrate the feasibility of establishing new chemical approaches towards modifications of amyloidogenic peptides (e.g., A β) by transition metal complexes designed based on their coordination and photophysical properties. In general, chemical modifications in peptides of interest can assist in furthering our understanding of principles in their properties, such as peptide assembly.

3.4. Experimental Section

3.4.1. Materials and Methods

All reagents were purchased from commercial suppliers and used as received unless otherwise noted. Analyses of small molecules by nuclear magnetic resonance (NMR) spectroscopy, Fourier-transform infrared (FT-IR) spectroscopy, and mass spectrometry (MS) were conducted on a Bruker AVANCE III HD NMR spectrometer, Varian Cary 620/670 FT-IR spectrometer (UNIST Central Research Facilities, Ulsan, Republic of Korea), and a Thermo Scientific Q Exactive Hybrid Quadrupole-Orbitrap Mass Spectrometer, respectively. A β_{40} , A β_{42} , and A β_{28} were purchased from Anygen (A β_{40} = DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV; A β_{42} = DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIA; Nam-myun, Jangseong-gun, Republic of Korea) and AnaSpec (A β_{28} = DAEFRHDSGYEVHHQKLVFFAEDVGSNK; Fremont, CA, USA), respectively. Double distilled H₂O was obtained from a Milli-Q Direct 16 system (Merck KGaA, Darmstadt, Germany). 1 sun light (100 mWcm⁻²) was treated from a Newport IQE-200 solar simulator (Irvine, CA, USA). Anaerobic reactions were performed in a N₂-filled glovebox (Korea Kiyon, Bucheon-si, Gyeonggi-do, Republic of Korea). Transmission electron microscopical images were taken by a JEOL JEM-2100 transmission electron microscope (UNIST Central Research Facilities, Ulsan, Republic of Korea). Analysis by electrospray ionization-ion mobility-mass spectrometry (ESI-IM-MS) was carried out using a Waters Synapt G2-Si quadrupole time-of-flight ion mobility mass spectrometer (DGIST Center for Core Research Facilities, Daegu, Republic of Korea) equipped with an ESI source. Photophysical properties were measured by a Shimadzu UV-2600 UV-visible (UV-Vis) spectrophotometer and a Varian Cary Eclipse fluorescence spectrophotometer (UNIST Central Research Facilities, Ulsan, Republic of Korea). Time-correlated single photon counting (TCSPC) was conducted for lifetime measurements with Ti:sapphire laser Mira900 (Coherent, Santa Clara, CA, USA), monochromator Acton Series SP-2150i (Princeton Instruments, Acton, MA, USA), and TCSPC module PicoHarp 300 (PicoQuant, Berlin, Germany), with micro channel plate photomultiplier tube (MCP-PMT) R3809U-59 (Hamamatsu, Shizuoka-ken, Japan) and fitted by PicoQuant FluoFit software (UNIST Central Research Facilities, Ulsan, Republic of Korea). A SpectraMax M5e microplate reader (Molecular Devices, Sunnyvale, CA, USA) was used to measure the absorbance for the MTT assay.

3.4.2. Synthesis of Ir(III) Complexes

3.4.2.1. Preparation of 2-Me

2-Me was synthesized by modifications of previously reported procedures.⁶³ $\text{CH}_3(\text{CH}_2)_3\text{Li}$ (*n*-BuLi; 2.5 M; 7.0 mL, 18 mmol) was slowly dropped to a solution of 4-bromotoluene (**1-Me**; 2.0 g, 12 mmol) in tetrahydrofuran (THF) under -78°C , and the solution was vigorously stirred for 1 h. $\text{B}(\text{OCH}_3)_3$ (2.2 g, 21 mmol) was slowly added to the solution, and the reaction mixture was stirred for additional 4 h. The reaction mixture was quenched with H_2O . The product was extracted with CH_2Cl_2 three times. The collected organic solution was treated with MgSO_4 and removed under the reduced pressure to obtain a white powder product. (1.2 g, yield 64%). ^1H NMR [400 MHz, CDCl_3 , δ (ppm)]: 8.13 (d, $J = 7.9$ Hz, 2H), 7.31 (d, $J = 7.5$ Hz, 2H), 2.45 (s, 3H).

3.4.2.2. Preparation of 2-F

2-F was synthesized by the same procedure as **2-Me** using 4-fluoriodobenzene (**1-F**; 3.0 g, 14 mmol), *n*-BuLi (2.5 M; 8.1 mL, 20 mmol), and $\text{B}(\text{OCH}_3)_3$ (2.5 g, 24 mmol) (white powder; 820 mg, yield 43%).⁶³ ^1H NMR [400 MHz, CDCl_3 , δ (ppm)]: 8.19-8.24 (m, 2H), 7.19 (t, $J = 8.8$ Hz, 2H).

3.4.2.3. Preparation of 3-H

3-H was synthesized by modifications of previously reported procedures.⁶⁴ 2-Chloroquinoline (400 mg, 2.4 mmol), phenylboronic acid (**2-H**; 358 mg, 2.9 mmol), and $\text{Pd}(\text{PPh}_3)_4$ (141 mg, 0.12 mmol) were added to a mixture of degassed THF and K_2CO_3 (2 M, aq) (1:1). The solution was refluxed under N_2 (g) overnight. After cooling down to room temperature, the solution was concentrated, and H_2O was added into the resulting solution. The organic phase was extracted with ethyl acetate (EtOAc) three times. The collected organic solution was treated with MgSO_4 and removed under the reduced pressure. The crude materials were purified by column chromatography (SiO_2 , 10:1 hexanes:EtOAc, $R_f = 0.6$; white powder; 297 mg, yield 59%). ^1H NMR [400 MHz, $\text{DMSO}-d_6$, δ (ppm)]: 8.45 (d, $J = 8.8$ Hz, 1H), 8.26 (d, $J = 7.2$ Hz, 2H), 8.14 (d, $J = 8.0$ Hz, 1H), 8.06 (d, $J = 8.0$ Hz, 1H), 7.98 (d, $J = 8.0$ Hz, 1H), 7.77 (t, $J = 7.2$ Hz, 1H), 7.46-7.62 (m, 4H).

3.4.2.4. Preparation of 3-Me

3-Me was synthesized by the same procedure as **3-H** using 2-chloroquinoline (600 mg, 3.7 mmol), **2-Me** (600 mg, 4.4 mmol), and $\text{Pd}(\text{PPh}_3)_4$ (212 mg, 0.18 mmol) (10:1 hexanes:EtOAc, $R_f = 0.6$; white powder; 733 mg, yield 91%). ^1H NMR [400 MHz, $\text{DMSO}-d_6$, δ (ppm)]: 8.18 (t, $J = 9.2$ Hz, 2H), 8.08 (d, $J = 8.0$ Hz, 2H), 7.86 (d, $J = 8.4$ Hz, 1H), 7.82 (dd, $J = 8.1, 1.5$ Hz, 1H), 7.72 (ddd, $J = 8.4, 6.9, 1.5$ Hz, 1H), 7.52 (ddd, $J = 8.1, 6.8, 1.2$ Hz, 1H), 7.34 (d, $J = 8.1$ Hz, 2H), 2.44 (s, 3H). ^{13}C NMR [100 MHz, $\text{DMSO}-d_6$, δ (ppm)]: 157.3, 148.3, 139.4, 136.9, 136.7, 129.7, 129.6, 129.4, 127.5, 127.1, 126.8, 126.1, 118.9, 21.4. FT-IR (neat cm^{-1}): 3055, 3026, 2958, 2914, 2858, 1597, 1552, 1496, 1431, 1373, 1319, 1288, 1244, 1213, 1184, 1157, 1126, 1111, 1053, 1016, 974, 949, 814, 789, 746, 717. HRMS for $[\text{C}_{16}\text{H}_{13}\text{N} + \text{H}]^+$ Calcd, 220.1121; found, 220.1116.

3.4.2.5. Preparation of 3-F

3-F was synthesized by the same procedure as **3-H** using 2-chloroquinoline (500 mg, 3.1 mmol), **2-F** (500 mg, 3.6 mmol), and Pd(PPh₃)₄ (176 mg, 0.15 mmol) (10:1 hexanes:EtOAc, *R_f* = 0.7; white powder; 616 mg, yield 90%). ¹H NMR [400 MHz, DMSO-*d*₆, δ (ppm)]: 8.22 (d, *J* = 8.4 Hz, 1H), 8.17 (t, *J* = 8.0 Hz, 3H), 7.83 (dd, *J* = 8.8 Hz, 2H), 7.73 (ddd, *J* = 8.5, 7.0, 1.5 Hz, 1H), 7.53 (ddd, *J* = 8.1, 6.8, 1.2 Hz, 1H), 7.21 (t, *J* = 8.8 Hz, 2H). ¹³C NMR [100 MHz, DMSO-*d*₆, δ (ppm)]: 168.8, 162.9, 160.4, 148.2, 143.8, 143.8, 143.3, 140.9, 131.7, 129.1, 129.0, 128.9, 127.7, 127.1, 125.9, 119.7, 119.6, 117.5, 109.5, 109.3. FT-IR (neat cm⁻¹): 3067, 1736, 1594, 1558, 1515, 1495, 1432, 1324, 1286, 1270, 1230, 1162, 1125, 1098, 1047, 1012, 977, 940, 852, 820, 789, 758, 710, 691, 673. HRMS for [C₁₅H₁₀FN + H]⁺ Calcd, 224.0870; found, 224.0864.

3.4.2.6. Preparation of 3-F2

3-F2 was synthesized by the same procedure as **3-H** using 2-chloroquinoline (860 mg, 5.3 mmol), 2,4-difluorophenylboronic acid (**2-F2**; 996 mg, 6.3 mmol), and Pd(PPh₃)₄ (304 mg, 0.26 mmol) (10:1 hexanes:EtOAc, *R_f* = 0.7; white powder; 742 mg, yield 59%). ¹H NMR [400 MHz, DMSO-*d*₆, δ (ppm)]: 8.46 (d, *J* = 8.8 Hz, 1H), 8.07-8.14 (m, 2H), 8.02 (d, *J* = 8.0 Hz, 1H), 7.88 (dd, *J* = 8.4, 2.4 Hz, 1H), 7.80 (t, *J* = 7.6 Hz, 1H), 7.63 (t, *J* = 7.6 Hz, 1H), 7.43 (t, *J* = 9.2 Hz, 1H), 7.28 (t, *J* = 8.8 Hz, 1H). ¹³C NMR [100 MHz, DMSO-*d*₆, δ (ppm)]: 164.5, 162.0, 159.5, 152.8, 148.0, 137.3, 133.2, 130.5, 129.5, 128.3, 127.3, 124.4, 122.3, 112.7, 105.1. FT-IR (neat cm⁻¹): 3057, 2954, 2923, 2853, 1676, 1613, 1596, 1497, 1456, 1430, 1418, 1318, 1294, 1264, 1134, 1096, 1053, 970, 942, 836, 808, 758. HRMS for [C₁₅H₉F₂N + H]⁺ Calcd, 242.0776; found, 242.0772.

3.4.2.7. Preparation of Ir-H

Ir-H was synthesized by modifications of previously reported methods.^{49,50} **3-H** (859 mg, 4.2 mmol) was added to a solution of IrCl₃·*n*H₂O (500 mg, 1.7 mmol) in a mixture of 2-methoxyethanol and H₂O (3:1). The solution was refluxed under N₂ (g) for 24 h. After cooling down to room temperature, brown precipitates were obtained by addition of H₂O. The crude product (the cyclometalated chloride-bridged Ir(III) dimer, [Ir(μ-Cl)(**3-H**)₂]₂) was washed with hexanes and cold diethyl ether (Et₂O) several times, dried, and used without further purification.⁴⁸

A solution of [Ir(μ-Cl)(**3-H**)₂]₂ (150 mg, 0.12 mmol) and AgOTf (91 mg, 0.35 mmol) was dissolved in a mixture of CH₂Cl₂ and CH₃OH (1:1). The solution was stirred under inert conditions for 6 h. The reaction mixture was filtered through Celite to remove precipitates. The filtrate was concentrated in vacuo, and the resultant residues were solidified with hexanes. The target product (orange powder; 41 mg, yield 22%) was collected by additional crystallization with CHCl₃ and hexanes. ¹H NMR [400

MHz, DMSO-*d*₆, δ (ppm)]: 9.12 (d, J = 8.8 Hz, 2H), 8.68 (d, J = 8.8 Hz, 2H), 8.46 (d, J = 8.8 Hz, 2H), 8.16 (d, J = 8.0 Hz, 2H), 7.96 (d, J = 7.6 Hz, 2H), 7.87 (t, J = 8.4 Hz, 2H), 7.73 (t, J = 7.2 Hz, 2H), 6.86 (t, J = 7.2 Hz, 2H), 6.55 (t, J = 7.2 Hz, 2H), 6.03 (d, J = 7.6 Hz, 2H).

3.4.2.8. Preparation of Ir-Me

Ir-Me was synthesized by the same procedure as **Ir-H** using **3-Me** (700 mg, 3.2 mmol), IrCl₃·*n*H₂O (433 mg, 1.5 mmol), [Ir(μ -Cl)(**3-Me**)₂]₂ (132 mg, 0.10 mmol), and AgOTf (77 mg, 0.30 mmol) (red powder; 72 mg, yield 44%). ¹H NMR [400 MHz, DMSO-*d*₆, δ (ppm)]: 9.06 (d, J = 8.4 Hz, 2H), 8.66 (d, J = 8.8 Hz, 2H), 8.41 (d, J = 8.8 Hz, 2H), 8.16 (dd, J = 8.1, 1.5 Hz, 2H), 7.83-7.90 (m, 4H), 7.72 (ddd, J = 8.0, 6.8, 1.1 Hz, 2H), 6.72 (d, J = 8.8 Hz, 2H), 5.89 (s, 2H), 1.85 (s, 6H). ¹³C NMR [100 MHz, DMSO-*d*₆, δ (ppm)]: 169.8, 148.4, 144.0, 141.5, 140.2, 139.1, 134.8, 131.2, 128.7, 127.5, 126.6, 126.5, 126.3, 123.0, 122.3, 119.1, 117.1, 21.2. FT-IR (neat cm⁻¹): 3361 (br), 3088, 2916, 1606, 1579, 1554, 1520, 1451, 1430, 1338, 1247, 1226, 1170, 1075, 1027, 988, 962, 876, 817, 785, 762, 734, 681, 662. HRMS for [M - 2H₂O - OTf]⁺ Calcd, 629.1563; found, 629.1564.

3.4.2.9. Preparation of Ir-F

Ir-F was synthesized by the same procedure as **Ir-H** using **3-F** (616 mg, 2.8 mmol), IrCl₃·*n*H₂O (358 mg, 1.2 mmol), [Ir(μ -Cl)(**3-F**)₂]₂ (134 mg, 0.10 mmol), and AgOTf (77 mg, 0.30 mmol) (orange powder; 67 mg, yield 41%). ¹H NMR [400 MHz, DMSO-*d*₆, δ (ppm)]: 9.08 (d, J = 8.8 Hz, 2H), 8.75 (d, J = 8.7 Hz, 2H), 8.50 (d, J = 8.8 Hz, 2H), 8.21 (dd, J = 8.1, 1.5 Hz, 2H), 8.12 (dd, J = 8.7, 5.9 Hz, 2H), 7.92 (ddd, J = 8.7, 6.8, 1.5 Hz, 2H), 7.78 (ddd, J = 8.0, 6.8, 1.1 Hz, 2H), 6.79 (td, J = 8.8, 2.6 Hz, 2H), 5.67 (dd, J = 9.9, 2.5 Hz, 2H). ¹³C NMR [100 MHz, DMSO-*d*₆, δ (ppm)]: 168.8, 162.9, 160.4, 148.2, 143.8, 143.8, 143.3, 140.9, 131.7, 129.1, 129.0, 128.9, 127.7, 127.1, 125.9, 122.3, 119.7, 119.6, 119.1, 117.5, 109.5, 109.3. FT-IR (neat cm⁻¹): 3359 (br), 3088, 2933, 2860, 1595, 1571, 1550, 1516, 1469, 1451, 1432, 1395, 1341, 1297, 1232, 1194, 1182, 1149, 1070, 1025, 980, 962, 889, 864, 847, 834, 804, 782, 744, 709, 675, 662. HRMS for [M - 2H₂O - OTf]⁺ Calcd, 637.1062; found, 637.1060.

3.4.2.10. Preparation of Ir-F2

Ir-F2 was synthesized by the same procedure as **Ir-H** using **3-F2** (927 mg, 3.8 mmol), IrCl₃·*n*H₂O (459 mg, 1.5 mmol), [Ir(μ -Cl)(**3-F2**)₂]₂ (100 mg, 0.071 mmol), and AgOTf (54 mg, 0.21 mmol) (orange powder; 18 mg, yield 15%). ¹H NMR [400 MHz, DMSO-*d*₆, δ (ppm)]: 8.89 (d, J = 8.8 Hz, 2H), 8.80 (d, J = 9.2 Hz, 2H), 8.51 (d, J = 9.2 Hz, 2H), 8.22 (d, J = 8.4 Hz, 2H), 7.92 (t, J = 7.2 Hz, 2H), 7.79 (t, J = 7.2 Hz, 2H), 6.86 (t, J = 11 Hz, 2H), 5.63 (d, J = 8.8 Hz, 2H). ¹³C NMR [100 MHz, DMSO-*d*₆, δ (ppm)]: 167.0, 166.9, 163.4, 162.4, 160.8, 160.7, 159.9, 159.8, 148.5, 145.3, 142.2, 137.6, 132.5, 132.0, 131.9, 131.2, 130.7, 129.4, 128.4, 128.0, 127.9, 127.5, 126.6, 122.8, 120.4, 120.2, 119.6, 117.3, 117.1, 99.7, 99.4, 99.1. FT-IR (neat cm⁻¹): 3319 (br), 3081, 2935, 1597, 1556, 1518, 1433, 1411, 1317, 1295,

1216, 1190, 1162, 1106, 1019, 992, 830, 756. HRMS for $[M - 2H_2O - OTf]^+$ Calcd, 673.0868; found, 673.0864.

3.4.3. Photophysical Properties of Ir(III) Complexes

Absorption and emission spectra of the solution of Ir(III) complexes (20 μ M in H_2O ; final 1% v/v DMSO) with or without histidine (His) or A β_{28} (200 μ M in H_2O) were recorded at 298 K by UV-Vis and fluorescence spectroscopy, respectively. Quantum yield (Φ) was calculated following previously reported procedures. $[Ir(2\text{-phenylquinoline})_2(2,2'\text{-bipyridine})]Cl$ ($\Phi_{ref} = 0.53$ in H_2O , 1% v/v DMSO) was used as a reference.⁴⁰ For lifetime measurements, time-correlated single photon counting (TCSPC) was performed. The second harmonic generation (SHG = 420 nm) of a tunable Ti:sapphire laser with ca. 150 fs pulse width and 76 MHz repetition rate was used as an excitation source. The emission was spectrally resolved by using some collection optics and a monochromator. The TCSPC module with an MCP-PMT was used for ultrafast detection. The total instrument response function (IRF) for measuring the fluorescence decay was less than 150 ps, and the temporal time resolution was less than 10 ps. The deconvolution of the actual fluorescence decay and IRF was fitted by using the FluoFit software to deduce the time constant associated with each exponential decay. Radiative decay constant (k_r) and nonradiative decay constant (k_{nr}) were calculated on the basis of previously reported equations.⁶⁵

3.4.4. Histidine Binding Affinities of Ir(III) Complexes

The solution of **Ir-Me**, **Ir-H**, **Ir-F**, or **Ir-F2** (20 μ M in H_2O , 1% v/v DMSO) with or without His (200 μ M) was measured by ESI-MS (Agilent 1200 and Bruker HCT). Dissociation constants (K_d) were determined through His titration experiments. Fluorescence intensity of the solution of **Ir-Me**, **Ir-H**, **Ir-F**, or **Ir-F2** (2 μ M in H_2O ; 1% v/v DMSO) with His (0-60 μ M) was measured after 2 h incubation without agitation at room temperature. The resultant titration points were fitted to the Hill's equation [$y = V_{max} \{x^n / (x^n + k^n)\}$] [V_{max} , emission intensity of complete saturation; n , cooperativity; k , half maximal effective concentration (EC_{50})] in non-linear curve fit (OriginPro 2015, OriginLab Corporation, Northampton, MA, USA) and the K_d values were calculated by the obtained constant [$K_d = k^n$].

3.4.5. Singlet Oxygen (1O_2) Generation by Ir(III) Complexes

The amounts of singlet oxygen (1O_2) generated upon treatment with **Ir-Me**, **Ir-H**, **Ir-F**, and **Ir-F2** were determined according to the method reported previously.⁴⁰ Solutions containing Ir(III) complexes (10 μ M in H_2O , 1% v/v DMSO) and 9,10-anthracenediyl-bis(methylene)dimalonic acid (ABDA as a 1O_2 substrate, 100 μ M) with or without His (10 μ M) were irradiated with 40% of 1 sun light (40 mWcm⁻²; optimized intensity for ABDA not to be degraded). The absorbance of ABDA was measured for 7.5 min with a 2.5 min interval.

3.4.6. Electrospray Ionization-Ion Mobility-Mass Spectrometry (ESI-IM-MS)

(i) [$A\beta_{40}$ (100 μM) with **Ir-Me**, **Ir-H**, **Ir-F**, or **Ir-F2** (500 μM)] and (ii) [$A\beta_{28}$ and/or $A\beta_{42}$ (100 μM) with **Ir-F** (100 μM)] upon 10 min exposure to 1 sun light were incubated in H_2O at 37 $^\circ\text{C}$ for 1 h without agitation. The incubated samples were diluted by 10 fold and then injected into a mass spectrometer. The capillary voltage, sampling cone voltage, and source temperature were set to 2.8 kV, 70 V, and 60 $^\circ\text{C}$, respectively. The backing pressure was adjusted to 3.2 mbar. Ion mobility wave height and velocity were adjusted to 10 V and 450 ms^{-1} , respectively, and gas flow for the helium cell and ion mobility cell was set to 120 and 30 mLmin^{-1} , respectively. Tandem MS (MS^2) analysis was additionally performed on the +3-charged [$A\beta_{40}$ + **Ir-F'**] ($m/z = 1656$) and singly oxidized $A\beta_{40}$ ($m/z = 1449$). The ESI parameters and experimental conditions were same as above. Collision-induced dissociation was conducted by applying the collision energy in the trap. More than 200 spectra were obtained for each sample and averaged for analysis.

3.4.7. $A\beta$ Aggregation Experiments

$A\beta$ experiments were conducted as previously published.¹⁹ $A\beta$ peptides were dissolved with ammonium hydroxide (NH_4OH , 1% v/v, aq), aliquoted, lyophilized, and stored at -80 $^\circ\text{C}$. A stock solution (ca. 200 μM) was prepared by re-dissolving $A\beta$ with NH_4OH (1% w/v, aq, 10 μL) followed by dilution with H_2O . The peptide concentration in solution was determined by measuring the absorbance of the solution at 280 nm ($\epsilon = 1450 \text{ M}^{-1}\text{cm}^{-1}$ for $A\beta_{40}$; $\epsilon = 1490 \text{ M}^{-1}\text{cm}^{-1}$ for $A\beta_{42}$ and $A\beta_{28}$). (i) For the inhibition experiments, $A\beta$ (25 μM ; H_2O) was first treated with Ir(III) complexes (i.e., **Ir-Me**, **Ir-H**, **Ir-F**, or **Ir-F2**; 250 μM ; 5% v/v final DMSO concentration) followed by exposure to 1 sun light for 10 min. The resulting samples were incubated at 37 $^\circ\text{C}$ for 24 h with constant agitation. (ii) For the disaggregation experiments, $A\beta$ (25 μM ; H_2O) was initially incubated at 37 $^\circ\text{C}$ for 2, 4, or 24 h with steady agitation. Ir(III) complexes (250 μM ; 5% v/v final DMSO concentration) were added to the preincubated $A\beta$ samples with or without 1 sun light for 10 min followed by an additional 4 h of incubation at 37 $^\circ\text{C}$ with constant agitation. (iii) For $A\beta_{28}$ experiments, $A\beta_{28}$ (50 μM ; H_2O) was treated with **Ir-F** (10 μM ; 1% v/v final DMSO concentration) and incubated at 37 $^\circ\text{C}$ for 1 h with steady agitation. $A\beta_{42}$ (20 μM ; H_2O) was treated to the $A\beta_{28}$ -**Ir-F'** sample followed by exposure to 1 sun light for 10 min. The resulting samples were incubated at 37 $^\circ\text{C}$ for 1 h with constant agitation. For the experiments under anaerobic conditions, all samples were prepared following the same procedure described above for the aerobic samples in a N_2 -filled glovebox.

3.4.8. Gel Electrophoresis with Western Blotting (Gel/Western Blot)

The resultant $A\beta$ species from both inhibition and disaggregation experiments were analyzed by gel electrophoresis followed by Western blotting (gel/Western blot) using an anti- $A\beta$ antibody (6E10;

Covance, Princeton, NJ, USA) or anti-A β_{42} antibody (Merck KGaA).¹⁹ Each sample (10 μ L) was separated using a 10–20% gradient Tris-tricine gel (Invitrogen, Grand Island, NY, USA). The gel was transferred to a nitrocellulose membrane and blocked with a bovine serum albumin (BSA) solution (3% w/v; Sigma, St. Louis, MO, USA) in Tris-buffered saline (TBS; Fisher, Pittsburgh, PA, USA) containing 0.1% Tween-20 (TBS-T; Sigma-Aldrich) for 3 h at room temperature. The membrane was treated with either an anti-A β antibody [6E10; 1:2,000] or an anti-A β_{42} antibody (1:2,000) in a solution of 2% BSA (w/v, in TBS-T) for 4 h at room temperature and then incubated with a horseradish peroxidase-conjugated goat anti-mouse secondary antibody (Cayman Chemical, Ann Arbor, MI, USA; 1:5,000) for 6E10-treated membranes or a horseradish peroxidase-conjugated anti-rabbit secondary antibody (Promega, Madison, WI, USA; 1:2,500) for anti-A β_{42} antibody-treated membranes in 2% BSA in TBS-T solution (w/v) for 1 h at room temperature. A self-made ECL solution (2.5 mM luminol, 0.20 mM *p*-coumaric acid, and 0.018% H₂O₂ in 100 mM Tris, pH 8.6) was used to visualize the results on a ChemiDoc MP Imaging System (BioRad, Hercules, CA, USA).

3.4.9. Transmission Electron Microscopy (TEM)

A β samples for TEM were prepared following the previously reported methods.¹⁹ Glow discharged grids (Formvar/Carbon 300-mesh; Electron Microscopy Sciences, Hatfield, PA, USA) were treated with the resultant A β (5 μ L) for 2 min at room temperature. Excess sample was removed with filter paper and the grids were washed with H₂O three times. Each grid was stained with uranyl acetate (1% w/v H₂O; 5 μ L) for 1 min. Uranyl acetate was blotted off and grids were dried for 20 min at room temperature. Images of samples were taken by a JEOL JEM-2100 transmission electron microscope (200 kV, 25000 \times magnification).

3.4.10. Cytotoxicity Studies

Mouse Neuro-2a (N2a) neuroblastoma cells were purchased from the American Type Cell Collection (ATCC, Manassas, VA, USA). Cells were maintained in the media containing 50% DMEM (GIBCO, Grand Island, NY, USA) and 50% opti-MEM (GIBCO), supplemented with 5% (v/v) fetal bovine serum (FBS; GIBCO), 1% (v/v) L-glutamine (GIBCO), 100 U/mL penicillin, and 100 mg/mL streptomycin (GIBCO). The cells were grown in a humidified atmosphere with 5% CO₂ at 37 °C. Cell viability was determined by the MTT assay [MTT = 3-(4,5-dimethyl-2-thiazolyl)-2,5-diphenyl-2*H*-tetrazolium bromide, Sigma-Aldrich]. The cells were seeded in a 96 well plate (15,000 cells in 100 μ L per well). (i) To identify the cytotoxicity of Ir(III) complexes, the cells were treated with their various concentrations (5, 10, 25, 50, or 100 μ M; 1% v/v final DMSO concentration) and incubated for 24 h. (ii) For the experiments with A β , A β (A β_{40} or A β_{42} ; final concentration, 20 μ M) was added with the Ir(III) complexes (final concentration, 5 μ M) exposed to 1 sun light for 10 min, and incubated for 24 h at

37 °C. The resultant A β species were treated with cells. After 24 h incubation, MTT [25 μ M; 5 mgmL⁻¹ in PBS (pH 7.4, GIBCO)] was incubated to each well and the plate was incubated for 3 h at 37 °C. Formazan produced by the cells was solubilized by addition of an acidic solution of *N,N*-dimethylformamide (DMF, 50% v/v, aq, pH 4.5) and sodium dodecyl sulfate (SDS, 20% w/v) overnight at room temperature in the dark. The absorbance was measured at 600 nm using a microplate reader. Cell viability was calculated relative to cells containing an equivalent amount of DMSO. Error bars were calculated as standard errors of mean (S.E.M.) from three independent experiments. For comparisons between two groups, Student's two-tailed unpaired *t* test was employed. Statistical difference was considered significant at **P* < 0.05.

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3.6. References

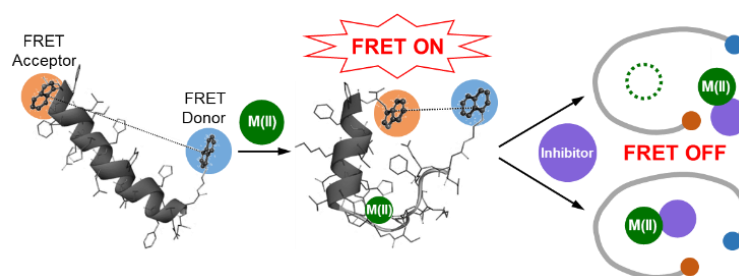
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Chapter 4.

Monitoring Metal–Amyloid- β Complexation by a FRET-based Probe: Design, Detection, and Inhibitor Screening



The results and results presented in this chapter were reported in the publication [Lee, H. J.;[†] Lee, Y. G.;[†] Kang, J.;[†] Yang, S. H.; Kim, J. H.; Ghisaidoobe, A. B. T.; Kang, H. J.; Lee, S.-R.; Lim, M. H.; Chung, S. J. *Chem. Sci.* **2019**, *10*, 1000–1007 ([†]equal contribution)]. Professor Sang J. Chung, Dr. Sang-Rae Lee, Professor Hyo Jin Kang, Young Geun Lee, Seung Hyun Yang, Ju Hwan Kim, and Amar B. T. Ghisaidoobe prepared **A-1**, measured its photophysical properties in the absence and presence of Zn(II) with data analysis, visualized possible binding modes between **A-1** and Zn(II) by modeling, and conducted inhibitor screening. Dr. Hyuck Jin Lee performed the FRET measurements and the mass spectrometric investigations with data analysis and TEM. I and Dr. Hyuck Jin Lee performed cell studies and analyzed the data. I and Dr. Hyuck Jin Lee wrote the manuscript with the guidance of Professor Mi Hee Lim.

4.1. Introduction

The number of aged people affected by neurodegenerative diseases has been increasing; however, the development of treatments for the diseases has not been successful due to the lack of understanding about their pathogenesis.^{1,2} The proposed risk factors of neurodegenerative diseases include metal ions [e.g., Zn(II)] and amyloidogenic peptides [e.g., amyloid- β (A β) and tau for Alzheimer's disease, α -synuclein for Parkinson's disease, and huntingtin for Huntington's disease].^{3–12} Toxic aggregates are formed upon aggregation of these amyloidogenic peptides, particularly in the presence of metal ions.^{2,13–15} The aggregation and conformational changes of such amyloidogenic peptides have been previously studied by luminescence, including Förster resonance energy transfer (FRET).^{16–21} In addition, the interactions between amyloidogenic peptides and metal ions (e.g., binding affinity and coordination geometry) have been investigated through multiple physical methods.^{8,9,22–26} Such approaches, however, require high concentrations of peptides and metal ions (e.g., high μ M) presenting significant challenge in performing the experiments due to the aggregation-prone properties of amyloidogenic peptides. Unfortunately, detecting the formation of metal-bound amyloidogenic peptides with a straightforward and efficient method (e.g., monitoring a turn-on signal) at a low concentration (ca. nM) has not been reported. Herein, we report a FRET-based probe (**A-1**; Figure 4.1 and Scheme 4.1), composed of A β _{1–21} grafted with a pair of FRET donor and acceptor, for monitoring metal–A β complexation at a nanomolar range with a turn-on FRET signal. The FRET intensity of **A-1** was observed to increase upon binding to Zn(II) (green; Figure 4.2). Note that although other metal ions [particularly, Cu(II)] are reported to interact with A β ,^{10,24} the use of our probe, **A-1**, is limited for paramagnetic metal ions, such as Cu(II), because its fluorescence is quenched (Figure 4.2). Additionally, the FRET signal of **A-1** was changed when (i) Zn(II) binding of **A-1** was interfered by the metal chelator, **EDTA** (ethylenediamine

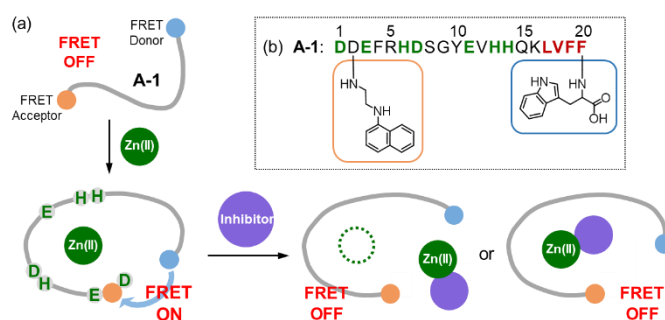
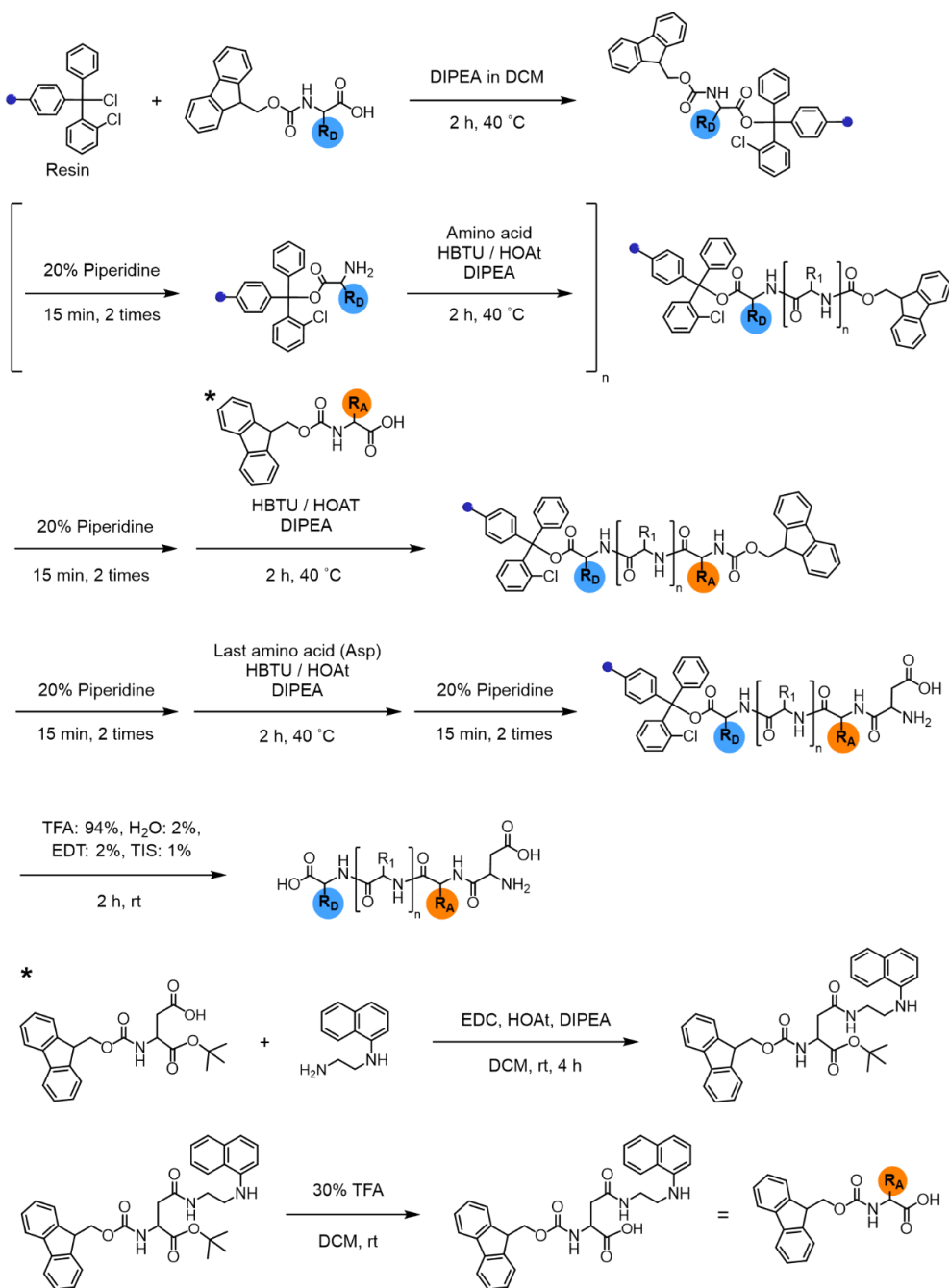
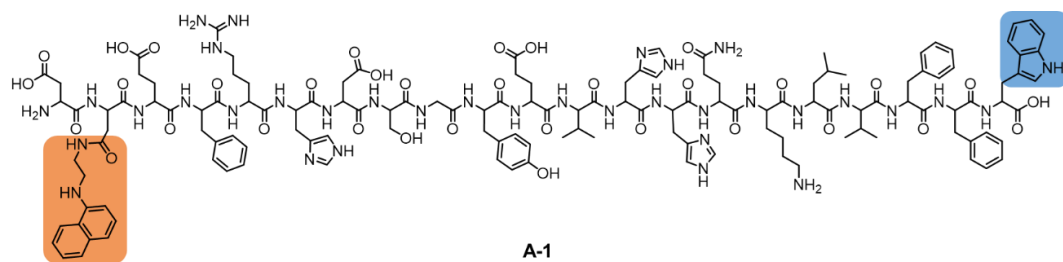


Figure 4.1. Design principle and sequence of the FRET-based probe, **A-1**. (a) FRET responses of **A-1** in the absence and presence of Zn(II) with and without inhibitors. (b) Amino acid sequence of **A-1**. **A-1** is composed of Trp (blue box) at the C-terminus as a FRET donor and 1-naphthylethylenediamine conjugated to the side chain of the Asp (orange box) at the N-terminus as a FRET acceptor. Proposed amino acid residues for metal binding and a portion of the self-recognition site are indicated in green and red, respectively.

Scheme 4.1. Synthetic routes to **A-1**.



tetraacetic acid),²⁹ or the compound, **L2-b** [*N*¹*N*¹-dimethyl-*N*⁴-(pyridin-2-ylmethyl)benzene-1,4-diamine],^{30,31} capable of forming a ternary complex with Zn(II)–A β ; (ii) the probe was aggregated. Moreover, a library of natural products as inhibitors against metal–A β interaction was screened based on the change in the FRET responses of Zn(II)-treated **A-1**. 8 out of 145 natural products were identified as effective inhibitors (> 80% inhibition) in vitro. Among the 8 molecules, 6 compounds were shown to lower the toxicity associated with Zn(II)–A β in living cells. Our studies demonstrate the feasibility of developing an efficient tactic to probe metal–amyloidogenic peptide complexation, along with its potential as a screening tool for drug discovery against neurodegenerative diseases.

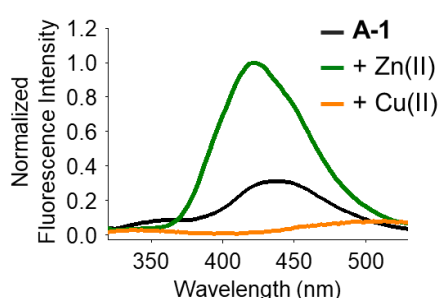


Figure 4.2. Fluorescent response of **A-1** (black) upon treatment with Zn(II) (green) or Cu(II) (orange). Conditions: [**A-1**] = 500 nM; [ZnCl₂] = 100 μ M; [CuCl₂] = 500 μ M; 10% DPBS; λ_{ex} = 280 nm; λ_{em} = 420 nm; room temperature.

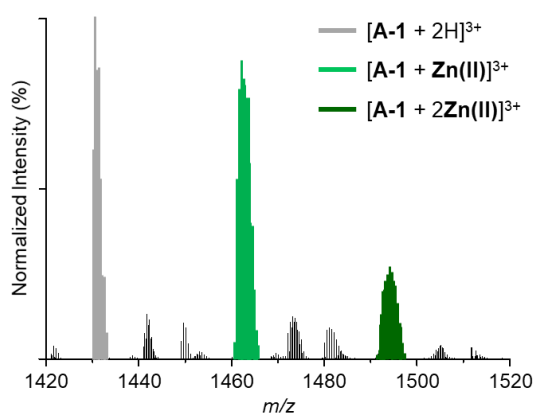


Figure 4.3. Zn(II) binding of **A-1**, monitored by MS. Conditions: [**A-1**] = 20 μ M; [ZnCl₂] = 2.0 mM; incubation for 1 h; 20 mM ammonium acetate, pH 7.4; room temperature; no agitation.

4.2. Results and Discussion

4.2.1. Design and Preparation of A-1

Our probe, **A-1**, was designed to have a FRET donor (Trp; $\lambda_{\text{ex}} = 280$ nm, $\lambda_{\text{em}} = 350$ nm) and an acceptor (1-naphthylethylenediamine conjugated to the side chain of an Asp; $\lambda_{\text{ex}} = 350$ nm, $\lambda_{\text{em}} = 420$ nm) for FRET at the C- and N-termini of the A β_{1-21} sequence, respectively (Figure 4.1). A β_{1-21} was selected as the main framework of **A-1** to include the metal binding site of A β (Figure 4.1b; proposed metal binding residues highlighted in green, e.g., Asp1, Glu3, His6, Asp7, Glu11, His13, and His14).^{10,26,32-35} Thus, **A-1** itself can interact with metal ions like A β . When **A-1** was treated with Zn(II), the Zn(II)–**A-1** complex was formed which was confirmed by mass spectrometry (MS) (Figure 4.3). Additionally, the binding affinity [$K_d = 5.6 (\pm 0.9)$ μM] of **A-1** (5 μM) for Zn(II) was measured by a fluorescence measurement (Figure 4.4a), similar to the K_d values of Zn(II)–A β obtained using the same method from previous studies.³⁶⁻³⁸ Moreover, the progression of peptide aggregation could be observed because **A-1** contains a portion of A β 's self-recognition site (Figure 4.1b; red, Leu17–Phe20).^{10,33,39} **A-1** was synthesized through solid phase peptide synthesis. The detailed synthetic routes are described in Scheme 4.1 and Experimental Section.

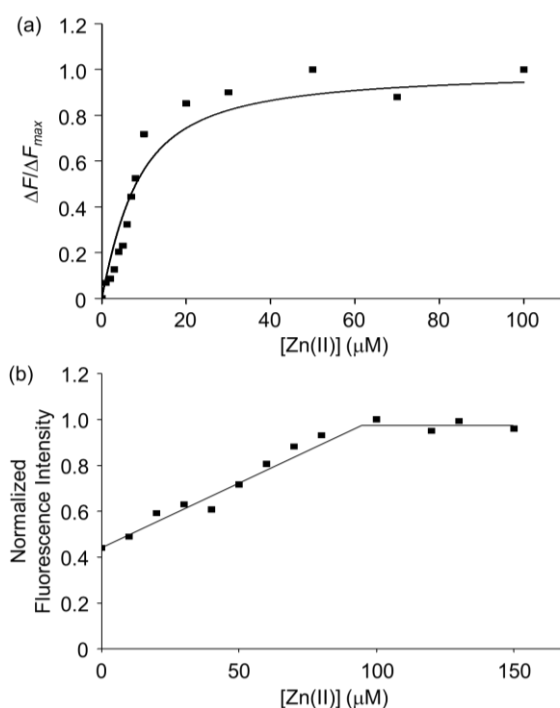


Figure 4.4. Variation of the FRET intensity of **A-1** (at 420 nm) upon titration with Zn(II). (a) Plot of $\Delta F/\Delta F_{\text{max}}$ of Zn(II)-bound **A-1** (5 μM) as a function of Zn(II) concentration. (b) Change in the fluorescence intensity of **A-1** (500 nM) upon treatment with various concentrations of Zn(II) at 420 nm. Conditions: [**A-1**] = 5 μM or 500 nM; [ZnCl_2] = 0–100 or 0–150 μM ; 10% DPBS; $\lambda_{\text{ex}} = 280$ nm; $\lambda_{\text{em}} = 420$ nm; room temperature.

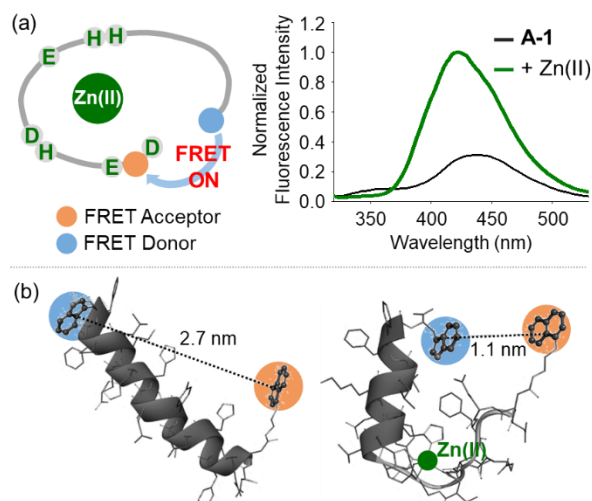


Figure 4.5. FRET response of **A-1** to Zn(II) and proposed structures of metal-free and Zn(II)-bound **A-1**. (a) Change in fluorescence upon incubation of **A-1** (black) with Zn(II) (green). Conditions: [**A-1**] = 0.5 μM ; [ZnCl_2] = 100 μM ; λ_{ex} = 280 nm. (b) Proposed structures of metal-free **A-1** (left) and Zn(II)-bound **A-1** (right). The structures were generated by modifications of the previously reported structures of metal-free A β (PDB: 1AMC)²⁷ and Zn(II)-bound A β (PDB: 1ZE9).²⁸ The approximate distances between the FRET donor and acceptor were indicated with dashed lines.

4.2.2. FRET Signal of **A-1** upon Zn(II) Binding

The presence of Zn(II) induced a significant turn-on FRET signal of **A-1** by > 2 fold compared to Zn(II)-free environment (Figure 4.5a). In order to minimize the aggregation of Zn(II)–**A-1** (vide infra; Figure 4.6), along with consideration of our probe's Zn(II) binding property, 250–500 nM of the probe and 100 μM of Zn(II) were used for this study. As shown in Figure 4.4b, the fluorescence intensity of **A-1** (500 nM) at 420 nm was enhanced upon titration and was saturated at ca. 100 μM of Zn(II). Since FRET occurs when a suitable donor and acceptor pair is in close proximity (1–10 nm) with the parallel orientation of the transition dipoles of the FRET donor and acceptor,^{40,41} an increase in the FRET intensity is indicative of **A-1**'s folding upon Zn(II) binding (Figure 4.5a). The possible conformations of metal-free and Zn(II)-bound **A-1** were visualized by modeling with modifications of the previously reported structures of metal-free A β and Zn(II)-bound A β (PDB: 1AMC²⁷ and 1ZE9,²⁸ respectively; Figure 4.5b). Without Zn(II), although the indole ring of the FRET donor and the naphthalene ring of the FRET acceptor are close enough for energy transfer (ca. 2.7 nm), they are not facing each other and shown to be unfavorable to have a dipole–dipole interaction for FRET (Figure 4.5b; left). Upon interacting with Zn(II), however, the indole and naphthalene rings become closer (ca. 1.1 nm) than those in metal-free **A-1** and are facing each other which could be favorable for the dipole–dipole interaction necessary for energy transfer, suggesting that an efficient FRET signal could be observed upon Zn(II) binding to the probe (Figure 4.5b; right). Additionally, the emission spectrum was blue shifted by ca. 25 nm possibly due to an environmental change of the FRET acceptor, naphthylamine, when **A-1** was

folded with Zn(II) treatment (Figure 4.5a; right). Note that we cannot rule out that intermolecular interactions resulted from **A-1**'s propensity to aggregate may induce the FRET.

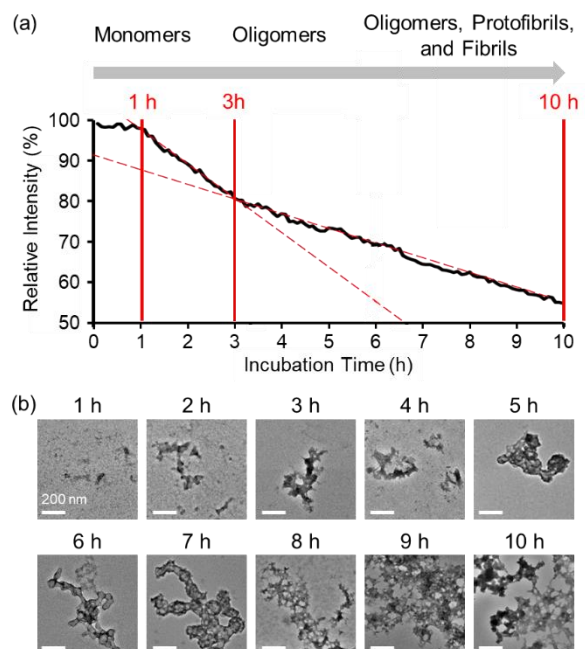


Figure 4.6. Time-dependent fluorescent response and aggregation progression of Zn(II)-treated **A-1**. (a) Change in the FRET signal of **A-1** with Zn(II) as a function of incubation time. (b) TEM images of Zn(II)-added **A-1** aggregates generated at various incubation time points (scale bar = 200 nm). Conditions: [**A-1**] = 0.25 μ M (for FRET) and 2.5 μ M (for TEM); [ZnCl₂] = 100 μ M (for FRET) and 1 mM (for TEM); λ_{ex} = 280 nm; λ_{em} = 420 nm; incubation up to 10 h; room temperature.

4.2.3. Aggregation of Zn(II)-bound **A-1**

In the absence of Zn(II), the FRET signal of **A-1** reduced as a function of incubation time (ca. 70% and ca. 85% decrease after 1 and 3 h incubation, respectively; Figure 4.7). This lowered signal may be triggered by the aggregation of **A-1** since the probe contains a portion of the self-recognition region of A β .^{10,33,39} In contrast, following incubation time, the FRET signal of Zn(II)-treated **A-1** decreased (ca. 2% and ca. 18% decrease after 1 and 3 h incubation, respectively; Figure 4.6a) at a slower rate compared to that of Zn(II)-free **A-1** (Figure 4.7). This indicates that the aggregation of **A-1** could be delayed by the presence of Zn(II), as observed with full-length A β_{40} (Figure 4.8). This difference could stem from the disparate conformations of A β aggregates generated upon the aggregation of metal-A β , distinct from those of metal-free A β .

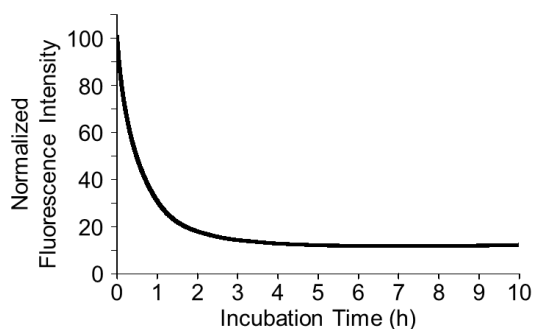


Figure 4.7. Change in the FRET signal of **A-1** following the incubation time without Zn(II). Conditions: $[A-1] = 300 \text{ nM}$; $\lambda_{\text{ex}} = 280 \text{ nm}$; $\lambda_{\text{em}} = 420 \text{ nm}$; incubation for 10 h; room temperature.

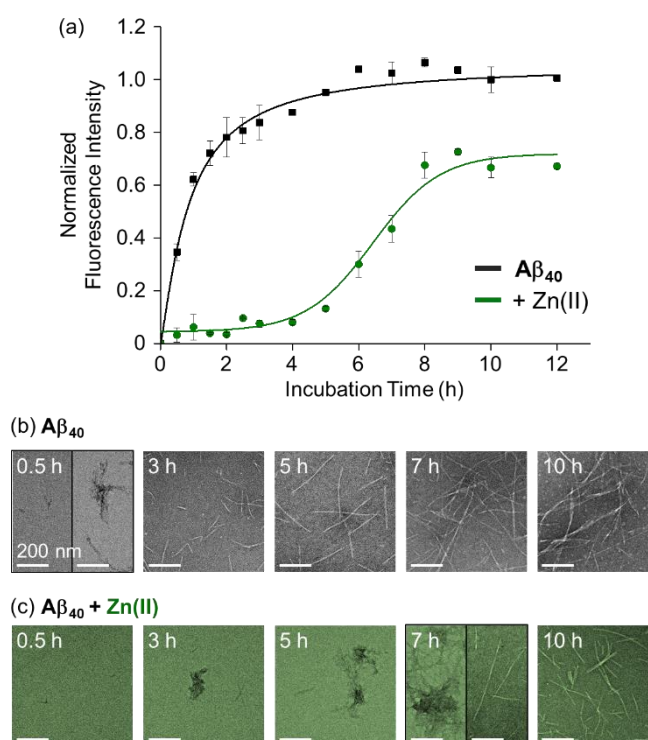


Figure 4.8. Time-dependent aggregation progression of $A\beta_{40}$ with and without Zn(II). (a) Aggregation kinetics of metal-free $A\beta_{40}$ and Zn(II)- $A\beta_{40}$, observed by the ThT assay. Conditions: $[A\beta_{40}] = 20 \text{ }\mu\text{M}$; $[ZnCl_2] = 20 \text{ }\mu\text{M}$; $[ThT] = 20 \text{ }\mu\text{M}$; pH 7.4; 37 °C; constant agitation. (b) Morphologies of $A\beta_{40}$ aggregates generated at various incubation time points, visualized by TEM (scale bar = 200 nm). Conditions: $[A\beta_{40}] = 20 \text{ }\mu\text{M}$; $[ZnCl_2] = 20 \text{ }\mu\text{M}$; pH 7.4; 37 °C; constant agitation.

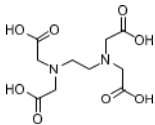
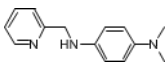
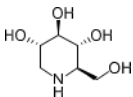
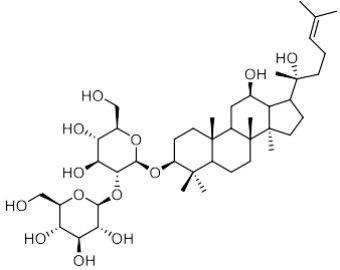
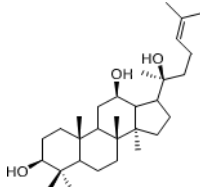
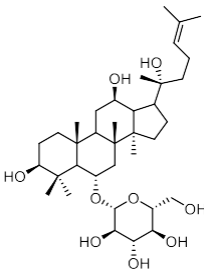
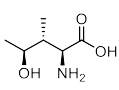
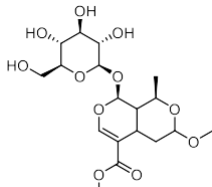
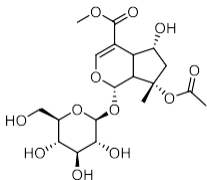
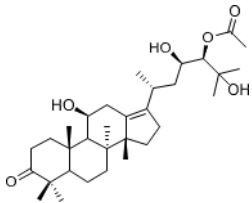
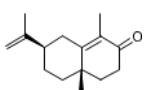
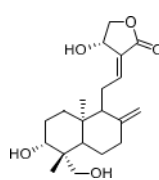
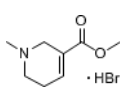
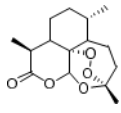
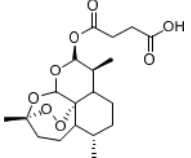
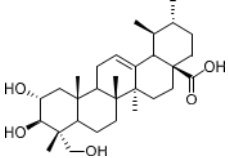
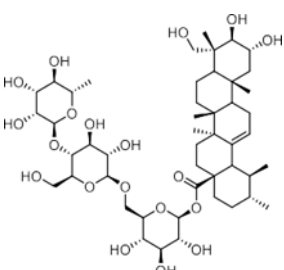
aggregates.^{28,42} Thus, we analyzed the morphologies of Zn(II)-**A-1** aggregates upon incubation by transmission electron microscopy (TEM). As depicted in Figure 4.6b, small and amorphous aggregates were observed after 1 h incubation of Zn(II)-added **A-1** followed by the detection of larger and more structured aggregates with longer incubation. Based on the variation of the FRET intensity as the probe

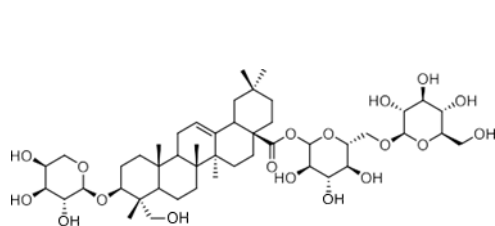
aggregated, the aggregation process of Zn(II)–**A-1** could be divided into three stages: (i) 0–1 h; (ii) 1–3 h; (iii) 3–10 h (Figure 4.6a). Up to 1 h incubation, the FRET signal of Zn(II)–**A-1** did not significantly decrease from the initial measurement. From 1 to 3 h, the FRET intensity of Zn(II)–**A-1** dropped drastically and after 3 h incubation, the FRET responses of Zn(II)–**A-1** were shown to be distinguishably reduced slower than those during the 1–3 h incubation period. This could be because Zn(II)–**A-1** formed large-sized aggregates, including protofibrils and fibrils, which might restrict its rotation to limit the distance between the FRET donor and acceptor, along with its solubility in aqueous media. Thus, our FRET-based probe, **A-1**, could monitor the progression of Zn(II)–A β aggregation, distinct from metal-free A β aggregation.

4.2.4. Screening Inhibitors against Zn(II)–A β Interaction

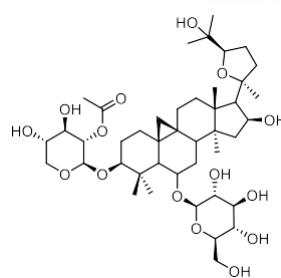
To evaluate whether Zn(II)-bound **A-1** is an effective identification tool for inhibitors against Zn(II)–A β interaction, alteration of the FRET signal of Zn(II)–**A-1** was monitored upon addition of the metal chelator (i.e., **EDTA**) or the molecule capable of forming a ternary complex with Zn(II)–A β (i.e., **L2-b**) (Table 4.1 and Figure 4.9a).^{29–31} When **EDTA** was introduced to Zn(II)–**A-1**, the FRET intensity was reduced by 83%, compared to the FRET signal of Zn(II)–**A-1**, and the emission spectrum was red shifted back to that observed under Zn(II)-free conditions (Figure 4.9, i). This suggests that Zn(II) was chelated out from **A-1** by **EDTA**, causing the probe to be unfolded. Furthermore, the treatment of **L2-b** to Zn(II)–**A-1** exhibited a noticeably weaker FRET signal than Zn(II)–**A-1** by 82%, but did not present the same emission spectrum as that of Zn(II)-free **A-1** (Figure 4.9a, ii). The fluorescence behavior of **L2-b**-added Zn(II)–**A-1** implies that a ternary complex [e.g., **L2-b**–Zn(II)–**A-1**] could be formed and thus Zn(II) still interacts with **A-1**, but the distance between the FRET donor and acceptor may not be in close proximity. Note that the emission of Trp was not significantly changed at ca. 350 nm which was not absorbed by the FRET acceptor upon addition of **EDTA** and **L2-b** (Figure 4.9a), indicating that the compounds did not affect the absorption and emission of the FRET donor. Together, our probe, **A-1**, demonstrates the ability to identify molecules with inhibitory activity towards metal–A β interaction.

Table 4.1. Chemical structures of **EDTA**, **L2-b**, and the natural products in our chemical library and their inhibition values (%) of the interaction between Zn(II) and **A-1**. The inhibition values (%) are presented in parenthesis.

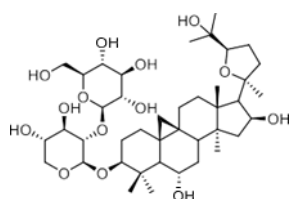
			
EDTA (83%)		L2-b (82%)	
			
1 (30%)	2 (40%)		3 (-24%)
			
4 (23%)	5 (-15%)	6 (42%)	7 (2.4%)
			
8 (53%)	9 (96%)	10 (57%)	11 (31%)
			
12 (48%)	13 (69%)	14 (28%)	15 (24%)



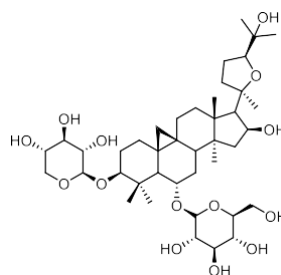
16 (17%)



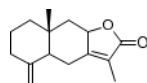
17 (37%)



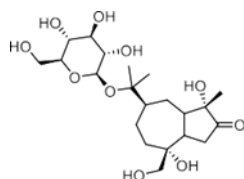
18 (-15%)



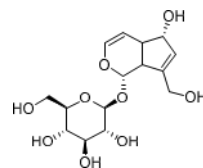
19 (66%)



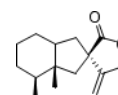
20 (76%)



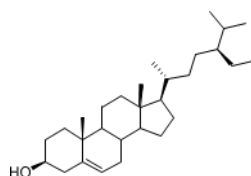
21 (54%)



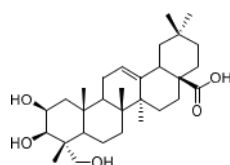
22 (40%)



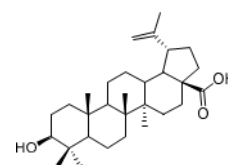
23 (33%)



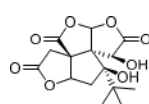
24 (23%)



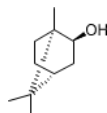
25 (2.4%)



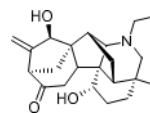
26 (-1.1%)



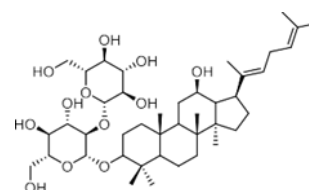
27 (37%)




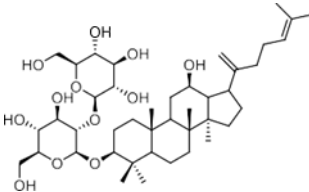
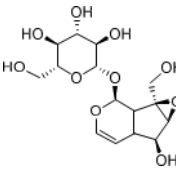
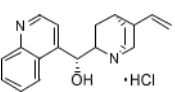

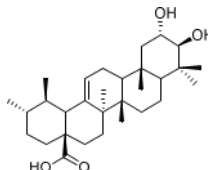
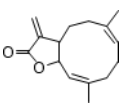
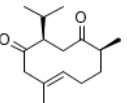
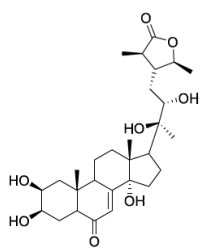
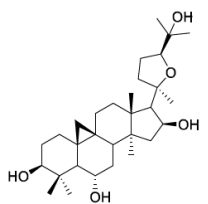
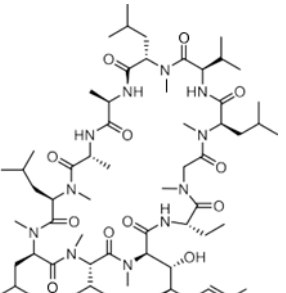
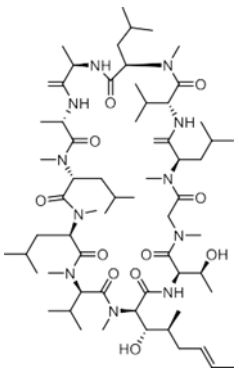
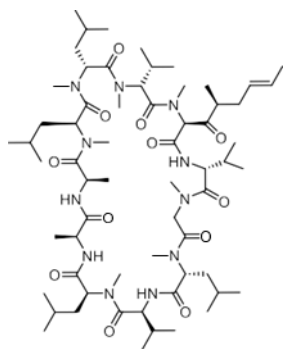
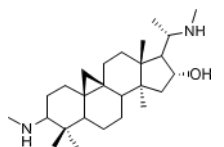
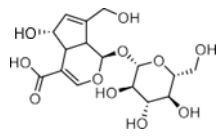
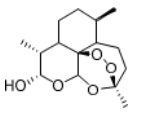
28 (31%)

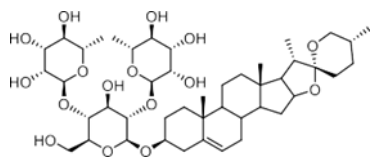


29 (44%)

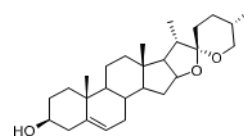


30 (68%)

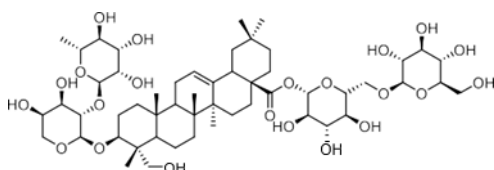
			
31 (49%)	32 (-19%)	33 (15%)	34 (44%)
			
35 (46%)	36 (-19%)	37 (110%)	38 (14%)
			
39 (19%)	40 (-13%)	41 (51%)	42 (-16%)
			
43 (52%)	44 (19%)	45 (53%)	46 (37%)



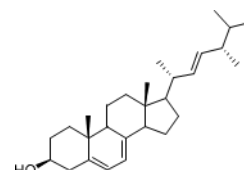
47 (-25%)



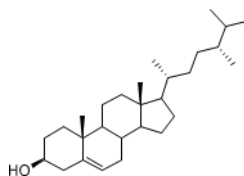
48 (3.9%)



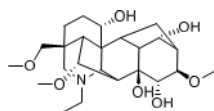
49 (2.8%)



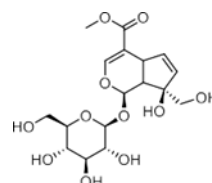
50 (46%)



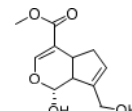
51 (17%)



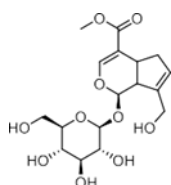
52 (27%)



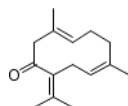
53 (25%)



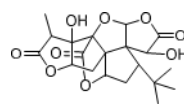
54 (67%)



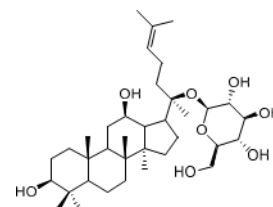
55 (28%)



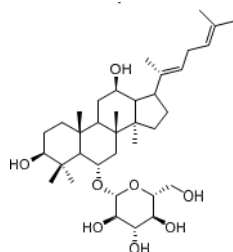
56 (54%)



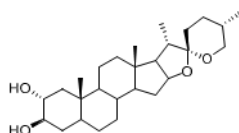
57 (23%)



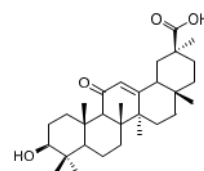
58 (36%)



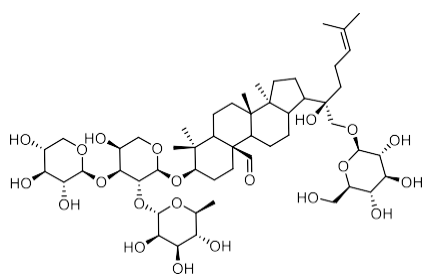
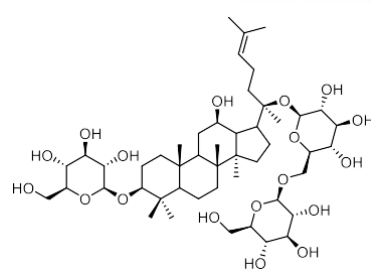
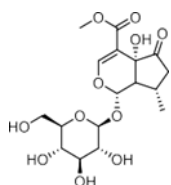
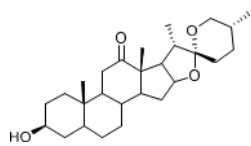
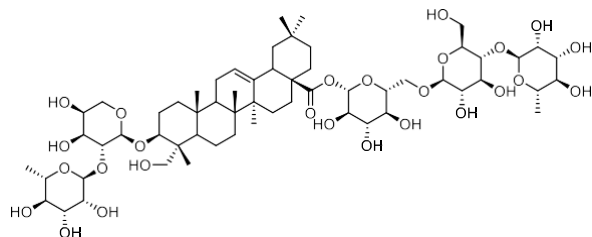
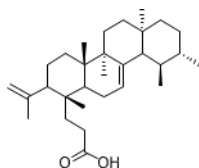
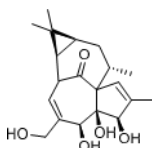
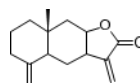
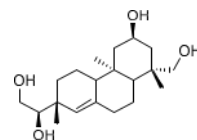
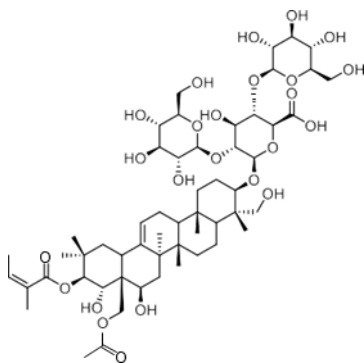
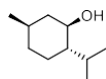
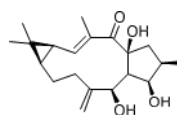
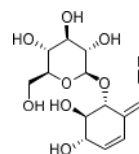
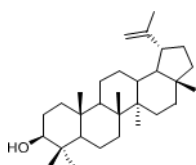
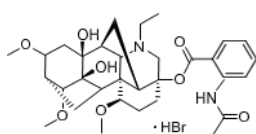
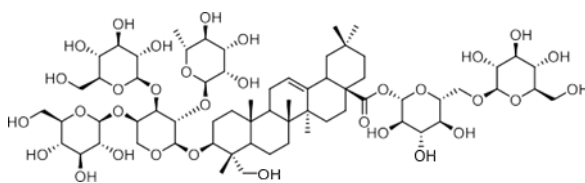
59 (35%)

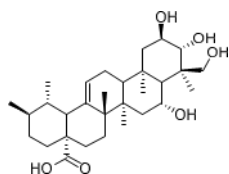
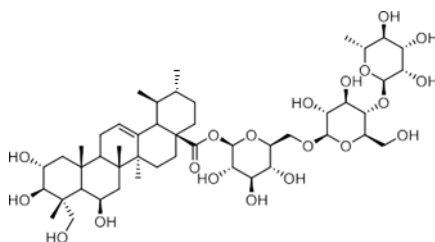
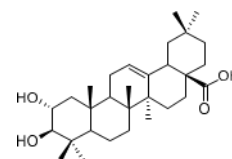
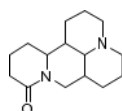
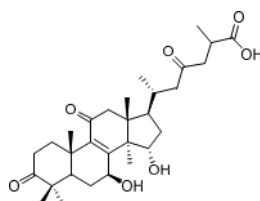
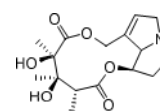
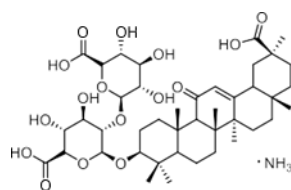
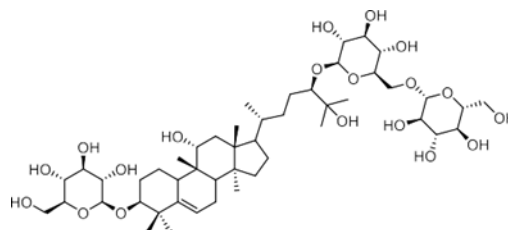
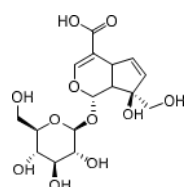
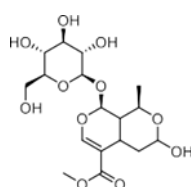
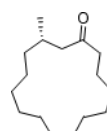
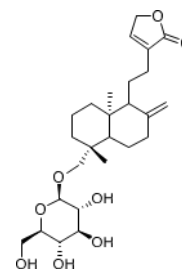
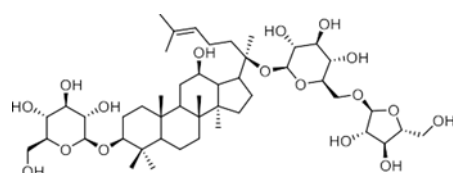
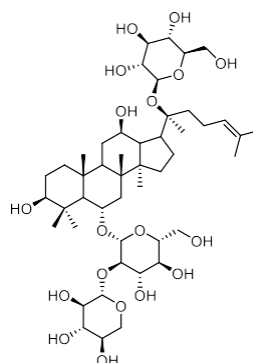


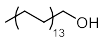
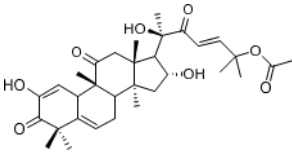
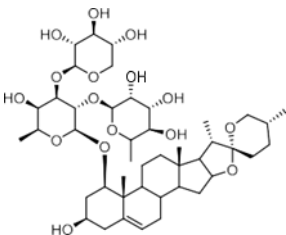
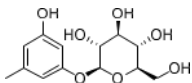
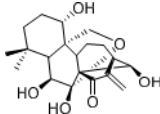
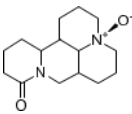

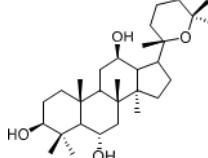
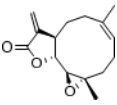
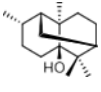
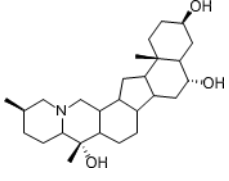
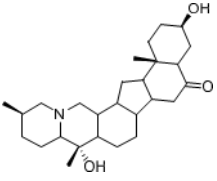
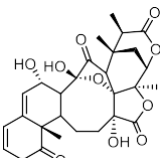
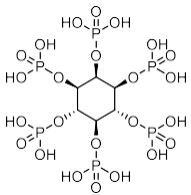
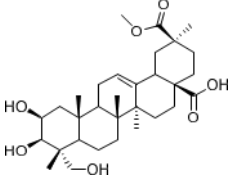
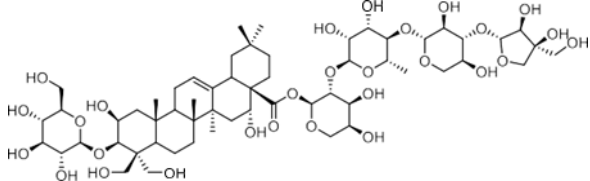
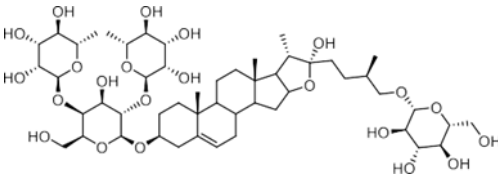
60 (51%)

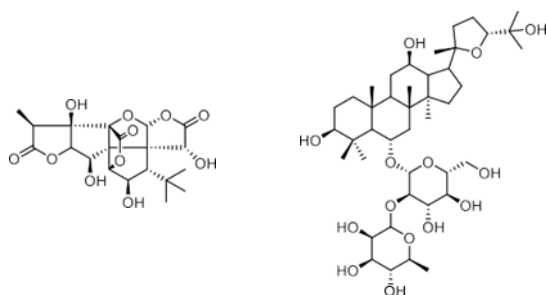


61 (100%)

**62** (39%)**63** (22%)**64** (22%)**65** (50%)**66** (-2.4%)**67** (6.8%)**68** (16%)**69** (54%)**70** (30%)**71** (86%)**72** (11%)**73** (100%)**74** (32%)**75** (-1.4%)**76** (35%)**77** (18%)

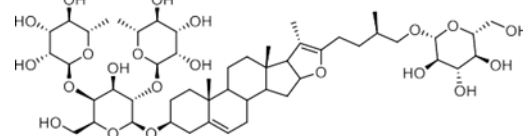
**78** (24%)**79** (9.6%)**80** (27%)**81** (22%)**82** (50%)**83** (21%)**84** (103%)**85** (22%)**86** (71%)**87** (32%)**88** (18%)**89** (37%)**90** (32%)**91** (13%)**92** (18%)

			
93 (21%)	94 (68%)	95 (-4.0%)	96 (31%)
			
97 (35%)	98 (18%)	99 (31%)	100 (0.30%)
			
101 (53%)	102 (-3.2%)	103 (12%)	
			
104 (33%)	105 (49%)	106 (99%)	107 (34%)
			
108 (16%)	109 (30%)		

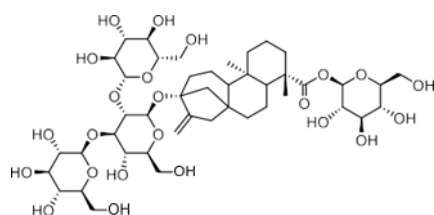


110 (14%)

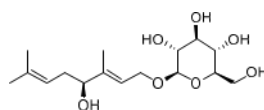
111 (32%)



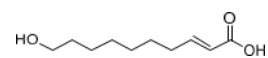
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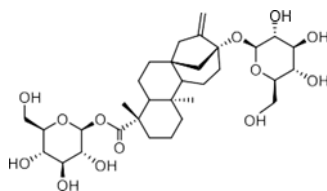
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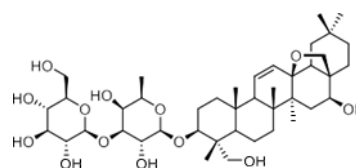
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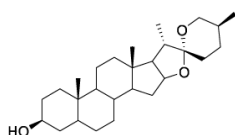
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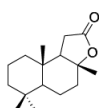
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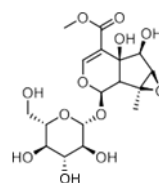
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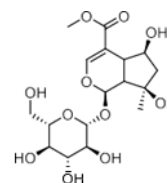
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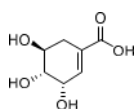
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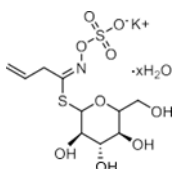
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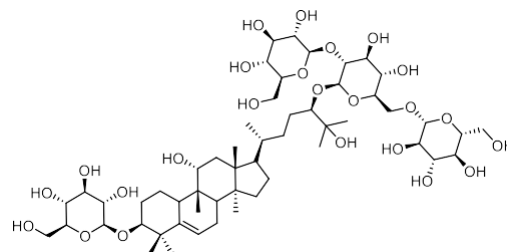
121 (16%)



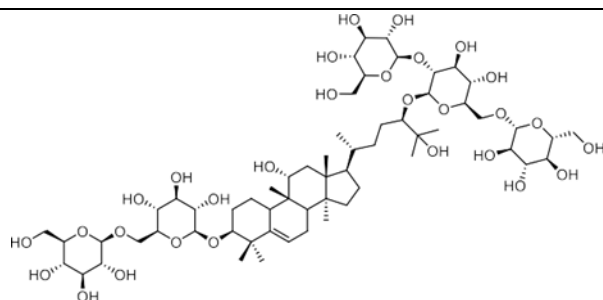
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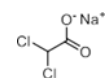
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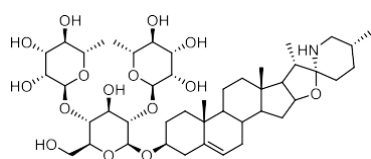
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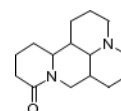
125 (12%)



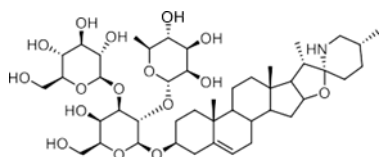
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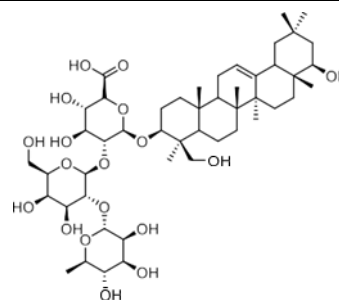
127 (-0.81%)



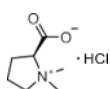
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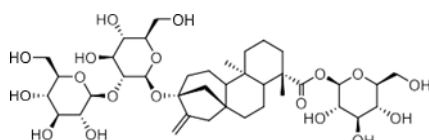
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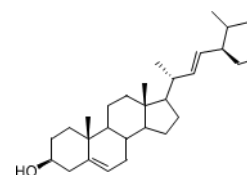
130 (-4.1%)



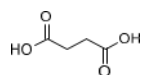
131 (33%)



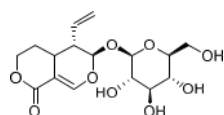
132 (33%)



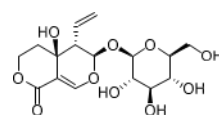
133 (56%)



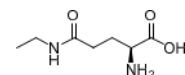
134 (51%)



135 (31%)



136 (31%)



137 (29%)

138 (19%)	139 (104%)	140 (9.9%)
141 (23%)	142 (33%)	143 (3.6%)
144 (38%)	145 (20%)	

Moving forward, to confirm the screening capability of our FRET-based method to verify molecules as potential inhibitors against metal–A β interaction, we built up a chemical library containing 145 natural products that do not absorb the FRET signal of Zn(II)–**A-1** at ca. 420 nm, similar to **EDTA** and **L2-b** (Figure 4.10 and Table 4.1). The FRET signal of Zn(II)–**A-1** upon addition of natural products was compared to that of Zn(II)–**A-1** to calculate % inhibition (Figures 4.9b, 4.11, and Table 4.1). In our library, (i) 15 molecules could not affect Zn(II) binding to **A-1**; (ii) 103 compounds showed 0 to 50% inhibition; (iii) 27 natural products induced a significant decrease in the fluorescence of Zn(II)–**A-1** by > ca. 50% (Figure 4.9b and Table 4.1). Furthermore, among the 27 natural products (> ca. 50% inhibition), 8 compounds (i.e., **9**, **37**, **61**, **71**, **73**, **84**, **106**, and **139**) demonstrated > 80% inhibitory activity against Zn(II)–**A-1** interaction. Three compounds (i.e., **61**, **71**, and **84** out of 8 potent inhibitors; Figure 4.9b and Table 4.1) contain both β -amyrin moiety and α,β -unsaturated carbonyl groups, previously reported for controlling metal–A β aggregation.⁴³ Note that the compounds containing an α,β -unsaturated carbonyl moiety could form a covalent adduct with A β possibly by reacting with Lys or His.^{44,45} To verify the covalent bond formation between one of the effective inhibitors, **61**, and an A β

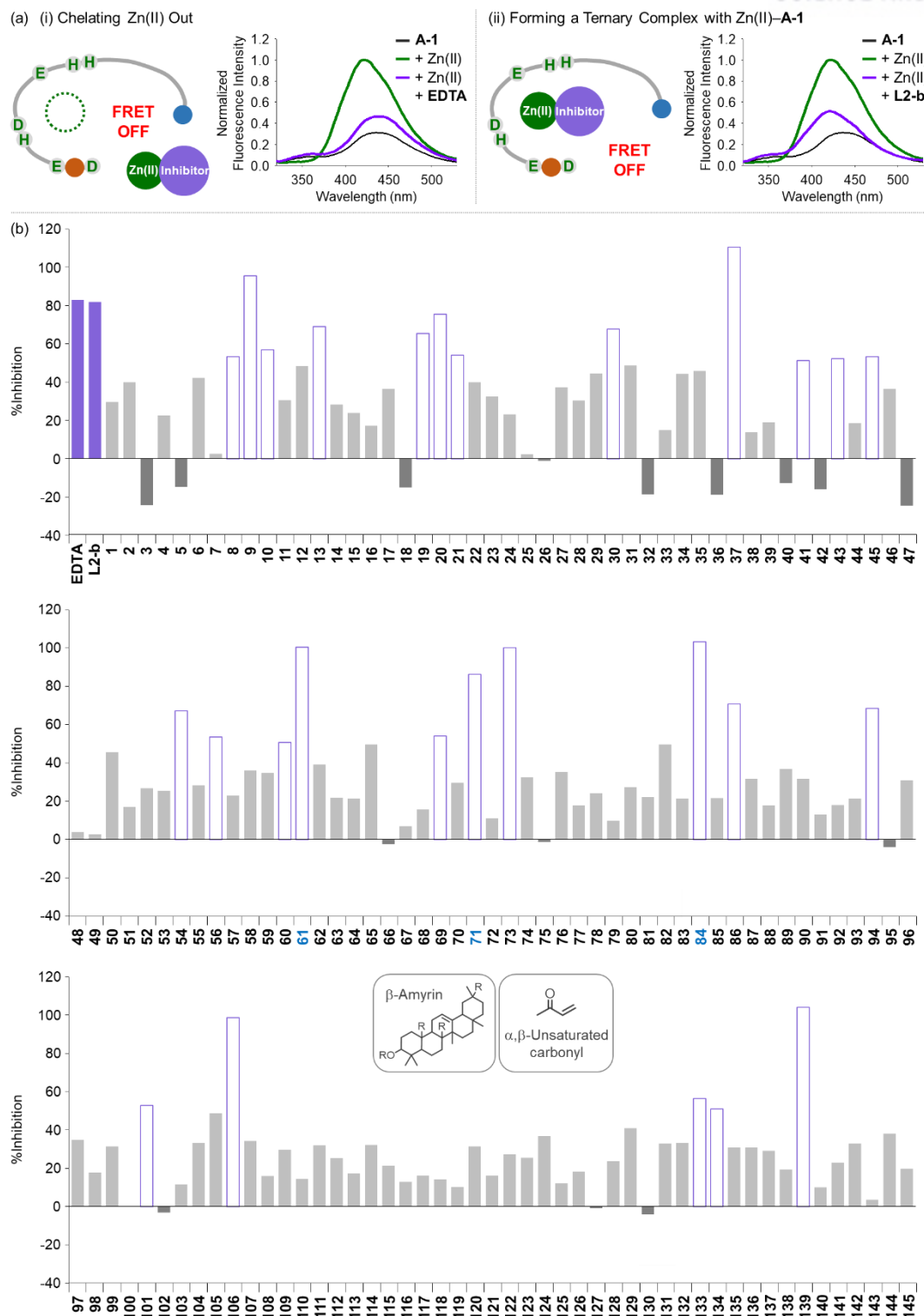


Figure 4.9. Change in the FRET signal of Zn(II)-bound **A-1** upon treatment with inhibitors against Zn(II)-A β interaction. (a) Fluorescent responses of **A-1** in the presence of both Zn(II) and compounds: [(i) EDTA and (ii) L2-b]. (b) Inhibition (%) of Zn(II)-**A-1** interaction by incubation with the natural products. Full data sets regarding the inhibition (%) of 145 natural products are summarized in Table 4.1. **61**, **71**, and **84** that contain both β -amyryn and α,β -unsaturated carbonyl groups and show > 80% inhibition against Zn(II)-**A-1** interaction are labeled in blue. Conditions: [**A-1**] = 0.3 μ M; [ZnCl₂] = 100 μ M; [inhibitor] = 100 μ M; incubation for 10 min; room temperature; λ_{ex} = 280 nm; λ_{em} = 420 nm.

fragment ($A\beta_{28}$), the sample containing **61** and $A\beta_{28}$ was monitored by MS. The MS measurement presented a covalent $A\beta_{28}$ –**61** adduct at 1244 m/z (blue peak; Figure 4.12a). In addition, the tandem MS analysis of the peak at 1244 m/z indicated $A\beta_{28}$ (at 1088 m/z) and **61** (at 471 m/z) confirming the formation of the covalent $A\beta_{28}$ –**61** adduct (Figure 4.12b). Thus, our inhibitors containing an α,β -unsaturated carbonyl moiety have the potential to bind **A-1**. Overall, inhibitors against Zn(II)– $A\beta$ interaction could be screened and identified by our probe, **A-1**, showing a variation in its FRET signal in the presence of Zn(II).

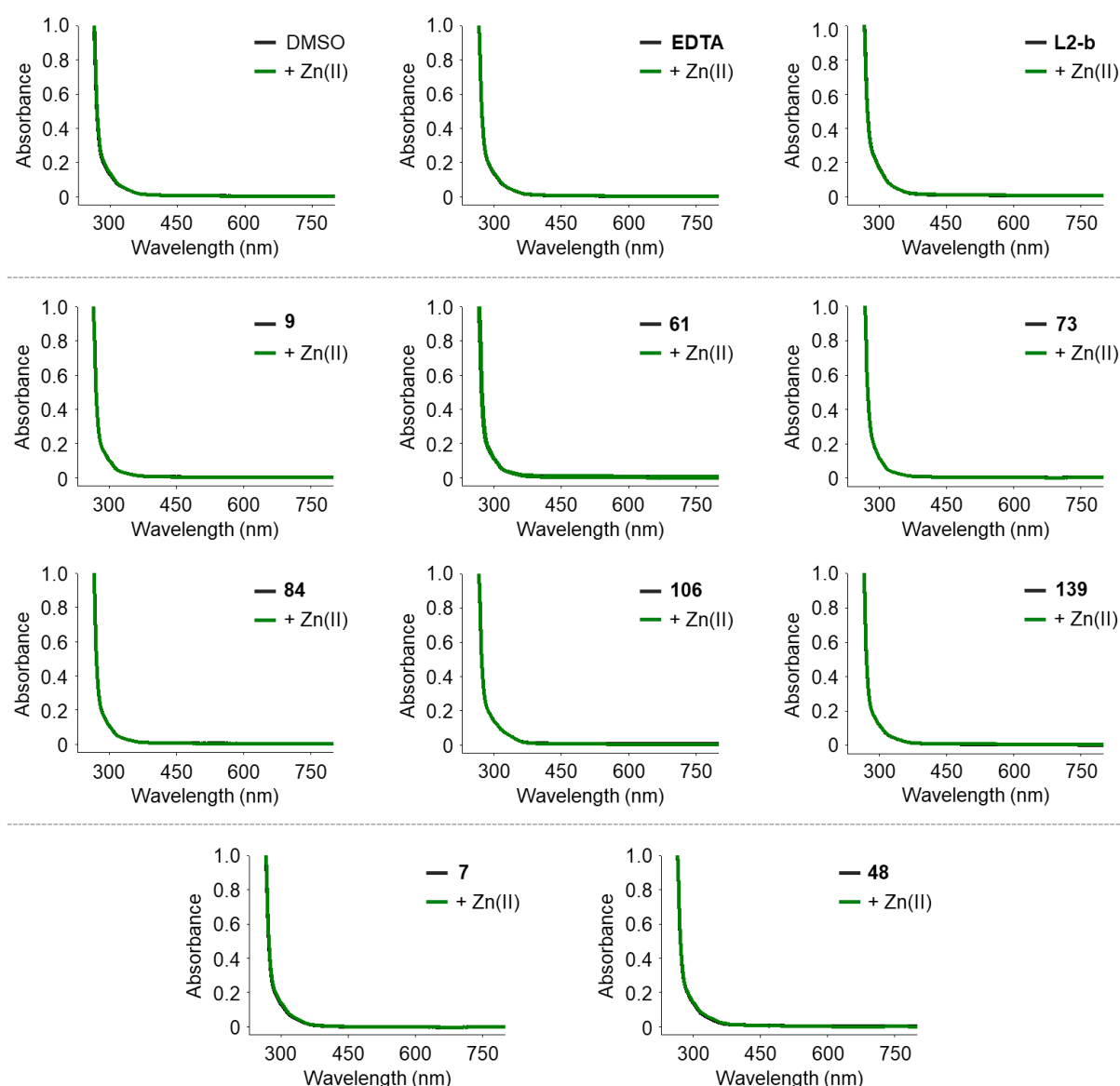


Figure 4.10. Absorption spectra of EDTA, L2-b, and the selected natural products in the absence (black) and presence (green) of Zn(II). Conditions: [compound] = 100 μ M; [ZnCl₂] = 100 μ M. Note that the absorption spectra were obtained by a microplate reader.

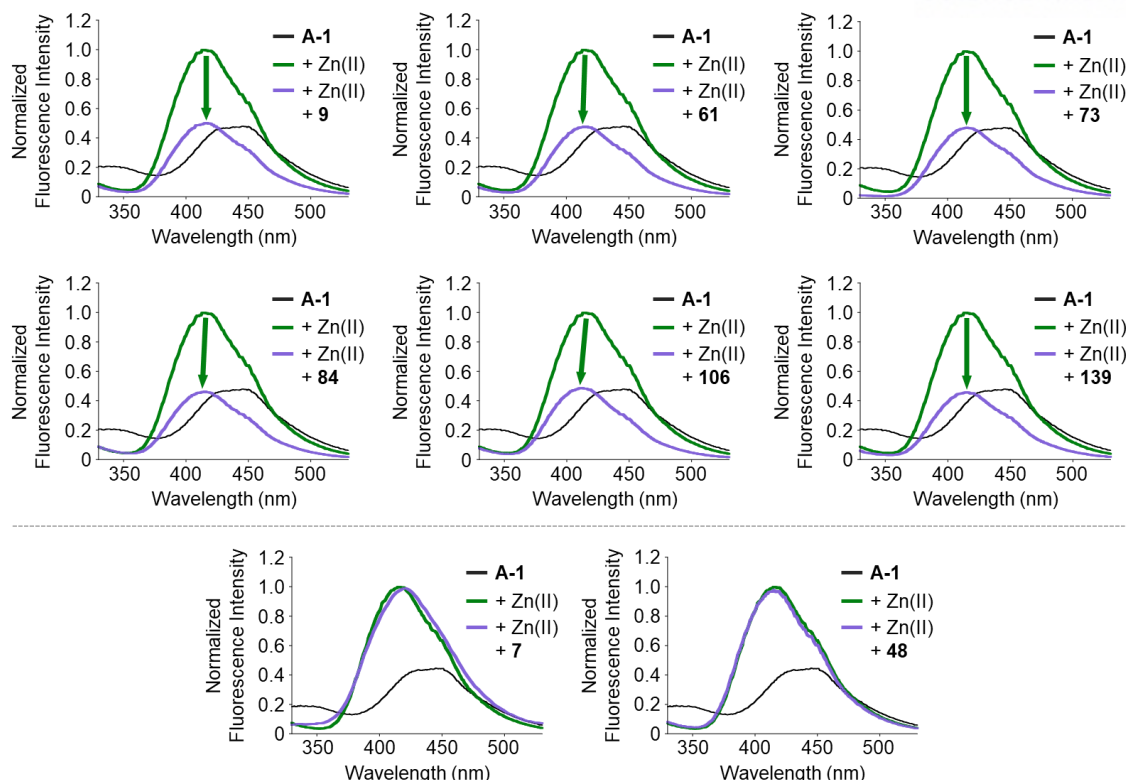


Figure 4.11. FRET responses of A-1 (black) to Zn(II) without (green) and with (purple) the selected natural products. The FRET intensities of the selected natural products showing noticeable inhibition (9, 61, 73, 84, 106, and 139) or no significant inhibition (7 and 48) against Zn(II)–A β interaction were monitored. Conditions: [A-1] = 300 nM; [ZnCl₂] = 100 μ M; [compound] = 100 μ M; λ_{ex} = 280 nm.

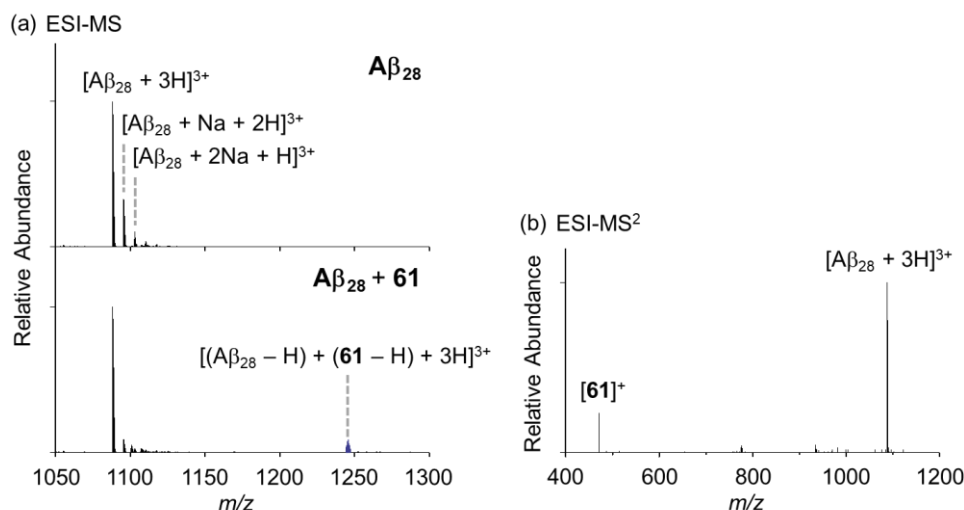


Figure 4.12. Mass spectrometric analysis of the sample containing A β_{28} with the natural product, **61**. (a) ESI-MS spectra of A β_{28} incubated without (top) and with (bottom) **61**. (b) Tandem MS (ESI-MS²) spectrum of the +3-charged A β_{28} –**61** complex (blue, [(A β_{28} – H) + (**61** – H) + 3H]³⁺, 1244 m/z). The ESI-MS² results support the formation of a covalent complex composed of A β_{28} and **61**. Conditions: [A β] = 5 μ M; [**61**] = 25 μ M; 20 mM ammonium acetate, pH 7.4; incubation for 2 h; room temperature; no agitation.

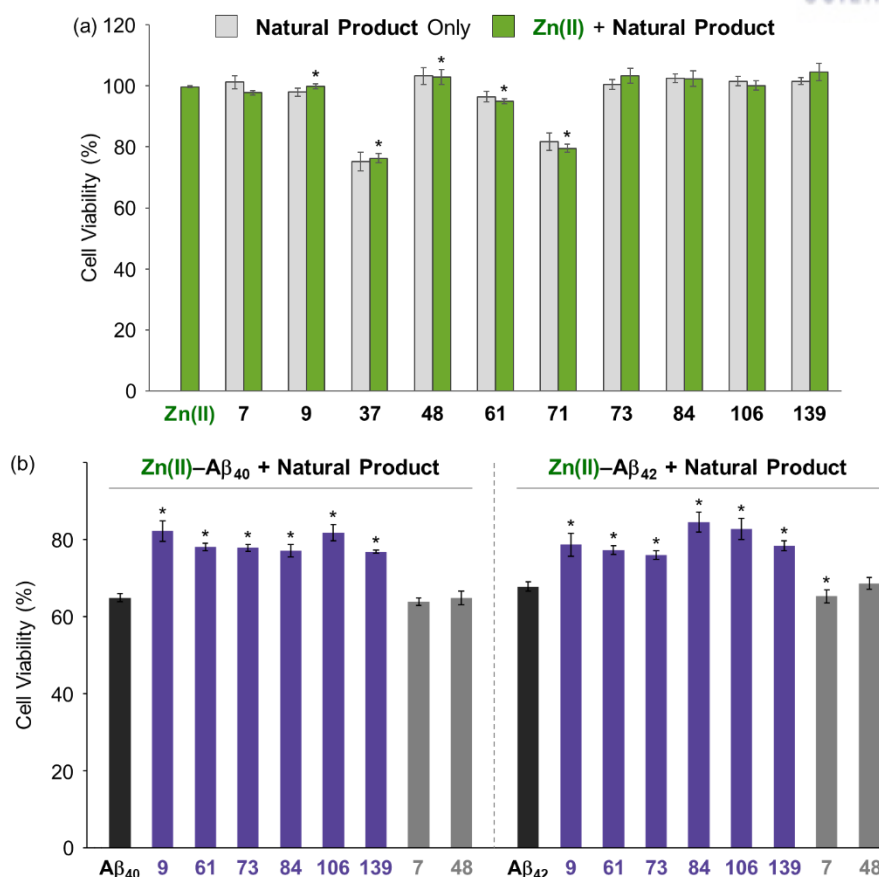


Figure 4.13. Effect of the selected natural products on the cytotoxicity triggered by Zn(II) and Zn(II)–Aβ. (a) Toxicity of the selected natural products with and without Zn(II) in 5Y cells. Cells were treated with compounds (10 μM) in the absence (light gray) and presence (light green) of Zn(II) (same equivalent to compounds; 10 μM) for 24 h at 37 °C. (b) Aβ₄₀ (left) or Aβ₄₂ (right; 10 μM) with Zn(II) (10 μM) was pre-incubated at room temperature for 1 h and then treated to 5Y cells with compounds (10 μM) for 24 h. Cell viability (%) was determined by the MTT assay compared to that obtained upon treatment with a volume of H₂O (1% v/v DMSO) equal to the samples added. Error bars represent the standard error of the mean from three independent experiments. * $P < 0.05$.

4.2.5. Influence of Inhibitors on Toxicity Associated with Zn(II) and Zn(II)–Aβ

The effect of the 8 natural products that showed > 80% inhibition against Zn(II)–A-1 interaction on the toxicity triggered by metal-free and Zn(II)-treated Aβ₄₀ and Aβ₄₂ (two major isoforms of Aβ)^{6,10} was determined in living cells. We first examined the toxicity of 10 natural products (i.e., 8 effective natural products: 9, 37, 61, 71, 73, 84, 106, and 139; 2 compounds which may not be able to disrupt Zn(II)–A-1 interaction: 7 and 48) in human neuroblastoma SH-SY5Y (5Y) cells. The tested compounds, except for 37 and 71, were not relatively toxic (> ca. 80% of cell viability at more than 10 μM) in the absence and presence of Zn(II) (Figures 4.13a and 4.14). Employing the relatively less toxic natural products (i.e., 7, 9, 48, 61, 73, 84, 106, and 139) with and without Zn(II), their impact on the toxicity induced by pre-incubated Aβ₄₀ and Aβ₄₂ with and without Zn(II) for 1 h at room temperature was analyzed. The natural products could not ameliorate the toxicity induced by metal-free Aβ (Figure 4.15). On the other

hand, as depicted in Figure 4.13b (purple), cell survival was improved by 6 natural products, determined as effective inhibitors against metal–A-1 interaction, even with the species of Zn(II)–A β . As expected, the compounds, **7** and **48**, shown to hinder Zn(II) binding to A β by less than ca. 5% (Figure 4.9b and Table 4.1), were not able to mitigate the toxicity induced by both metal-free and Zn(II)-associated A β (Figures 4.13b and 4.15; gray). Thus, our FRET-based method employing A-1 demonstrates its practical utility to determine molecules that can affect metal–A β interaction and, as a result, alleviate metal–A β -linked cytotoxicity.

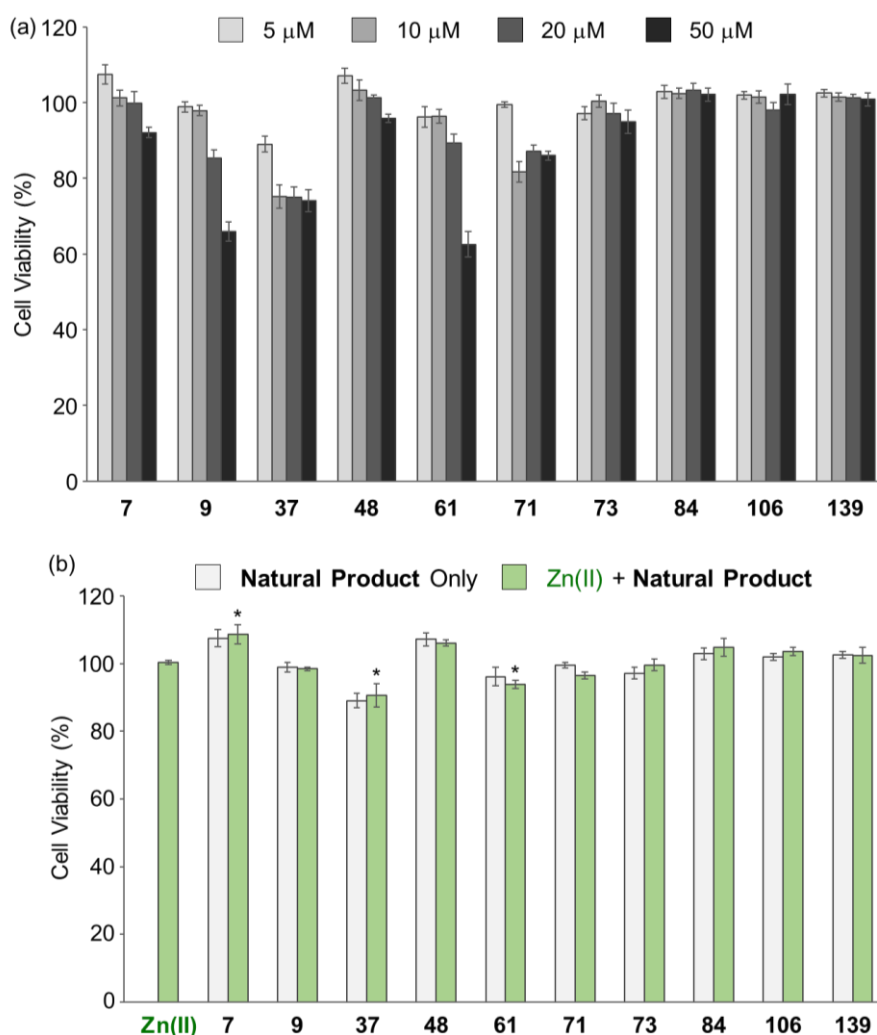


Figure 4.14. Toxicity of the selected natural products with and without Zn(II) in 5Y cells. (a) Cells were treated with various concentrations (5, 10, 20, and 50 μ M) of compounds for 24 h at 37 $^{\circ}$ C. (b) Compounds (5 μ M) in the absence (gray) and presence (green) of Zn(II) (same equivalent to the compounds; 5 μ M) were added to cells and incubated for 24 h at 37 $^{\circ}$ C. Cell viability (%) was determined by the MTT assay. The viability value was calculated compared to that of the cells added with DMSO only (1%, v/v). Error bars represent S.E.M. from three independent experiments. * $P < 0.05$ [versus Zn(II) or natural products].

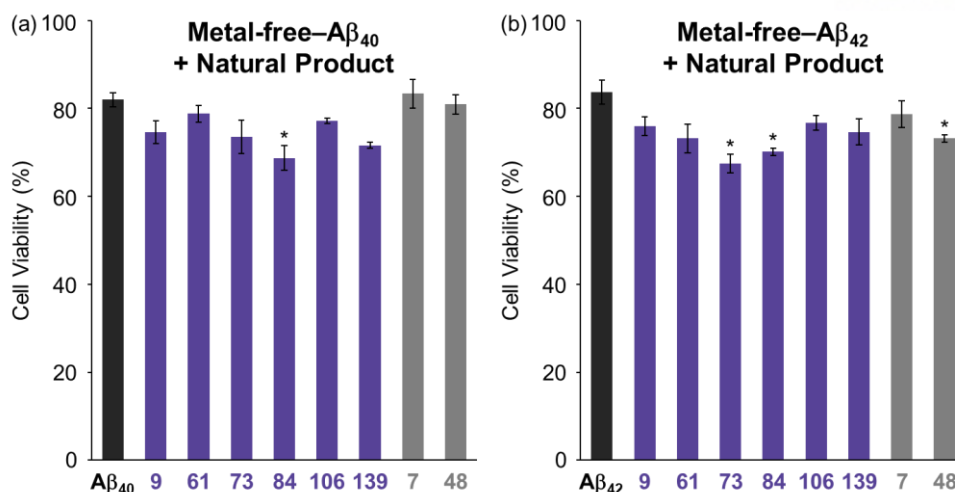


Figure 4.15. Effect of the selected natural products on the toxicity triggered by metal-free A β in 5Y cells. (a) A β ₄₀ or (b) A β ₄₂ (10 μ M) was pre-incubated at room temperature for 1 h and then treated to 5Y cells with compounds (10 μ M) for 24 h. Cell viability (%) was determined by the MTT assay compared to that of the cells treated with a volume of H₂O (1% v/v DMSO) equal to the samples added. Error bars represent S.E.M. from three independent experiments. * $P < 0.05$.

4.3. Conclusions

Since metal ions and amyloidogenic peptides (e.g., A β) can interact with each other and induce neurotoxicity, our understanding of such complexation is important to reveal their effects in the pathogenesis of neurodegenerative diseases. In order to verify the feasibility of monitoring metal–amyloidogenic peptide interactions, we employed A β as an example of amyloidogenic peptides to develop a FRET-based probe, **A-1**, to detect the metal binding of A β and the progression of metal–A β aggregation effectively and efficiently. Upon addition of Zn(II), the FRET signal of **A-1** was significantly increased due to the folding of our probe. In addition, when the probe aggregated with Zn(II), its fluorescent response was altered in a distinct manner from that of metal-free case. Furthermore, by utilizing our FRET-based probe to screen a chemical library (total 145 compounds), we identified 6 natural products capable of significantly modulating metal–A β interaction (> 80% inhibition) in vitro and diminishing cytotoxicity associated with Zn(II)–A β in living cells. Our overall studies illustrate the development of a strategy to monitor metal–A β interaction and its applicability towards searching potent inhibitors against metal–A β interaction. In the near future, for biological applications, new and optimized probes will be developed to monitor the interaction between A β and Zn(II) or other metal ions, including Cu(II), showing more sensitive fluorescent responses with lower energy profiles for excitation and emission (e.g., near-infrared region). Applying our tactic to other amyloidogenic peptides, their interactions with metal ions could be, and the inhibitors against metal–amyloidogenic peptide interaction could be identified.

4.4. Experimental Section

4.4.1. Materials and Methods

All chemical reagents (reagent grade) were purchased from Sigma Aldrich or Tokyo Chemical Industry (Tokyo, Japan) and used as received. Fmoc-protected amino acids were purchased from Chemimpex (Wood Dale, IL, USA) and GL biochem (Shanghai, China). Full length A β (i.e., A β ₄₀ and A β ₄₂) peptides were purchased from Anaspec (Fremont, CA, USA) (A β ₄₀ = DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVV; A β ₄₂ = DAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVV-A). Reaction products were analyzed using high performance liquid chromatography (HPLC), matrix associated laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS), and nuclear magnetic resonance spectroscopy (NMR). HPLC analysis was performed using the Waters photodiode array detector 996, separation module 2695, and XBridge™ C18 column (5 μ m, 4.6 x 250 mm). Peptide purification was performed by the Waters XBridge™ Prep C18 column (5 μ m, 19 x 250 mm). Purified peptide samples and their Zn(II) binding studies were analyzed by a Bruker MALDI-TOF mass spectrometer (Sogang University, Seoul, Republic of Korea) and a Q Exactive Plus Orbitrap mass spectrometer (Thermo Fisher Scientific, Waltham, MA, USA), respectively. Fluorescence was recorded on a PerkinElmer LS55 fluorescence spectrometer (PerkinElmer, Waltham, MA, USA) and HORIBA PTI QuantaMaster 8000 fluorescence spectrometer (HORIBA, Kyoto, Japan). TEM images were taken by a JEOL JEM-2100 transmission electron microscope [UNIST Central Research Facilities (UCRF), Ulsan, Republic of Korea] and a Tecnai F30 (FEI) transmission electron microscope [KAIST Analysis Center for Research Advancement (KARA), Daejeon, Republic of Korea]. Absorbance values of compounds and the MTT assay and the fluorescence intensity of ThT were measured using a Molecular Devices SpectraMax M5e microplate reader (Sunnyvale, CA, USA). The complex formation between A β fragments and the natural product was analyzed by the MicrOTOF-QII Hybrid Quadrupole-Time of Flight mass spectrometer (Bruker, Billerica, MA, USA) equipped with an ESI source [KARA, KAIST, Republic of Korea].

4.4.2. Synthesis and Purification of A-1

A-1 was synthesized through solid phase peptide synthesis (SPPS) using the 2-chlorotritylchloride resin (loading = 1.2 mmol/1 g resin). The resin was swelled with dry dichloromethane (DCM) for 30 min at room temperature. Immobilization of the Fmoc-amino acid was carried out on 1 g resin using 2 equiv of the Fmoc amino acid (2.4 mmol) and 4 equiv of *N,N*-diisopropylethylenediamine (DIPEA) for 1 h at room temperature. Fmoc deblocking was achieved twice for 10 min at room temperature using 20% (v/v) piperidine in *N,N*-dimethylformamide (DMF) followed by washing with DMF. Peptide coupling reactions were executed according to a pre-activation (10 min) protocol using 4 equiv of the appropriate amino acid, 4 equiv of 2-(1*H*-benzotriazol-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate (HBTU), 4 equiv of 1-hydroxy-benzotriazole (HOBt), and 8 equiv of DIPEA. Then, the preactivated

solution was added to the resin and allowed to shake for 2 h at 30 °C. Using the above protocol, the 21-mer peptide, **A-1** (DDnapEFRHDSGYEVHHQKLVEFFW), composed of natural amino acids and/or a side chain-modified aspartic acid with 1-naphthylethylenediamine (Dnap) was synthesized. Cleavage of the final peptide from the resin and deprotection of the acid-labile protective groups were accomplished using a mixture of trifluoroacetic acid (TFA), thioanisole, ethanedithiol, and double-distilled water (ddH₂O) (94/1/2.5/2.5, v/v/v/v). The crude peptide was precipitated from the cleavage solution and thoroughly washed with ice-cold diethyl ether (Et₂O). After preparative HPLC purification using a gradient of acetonitrile (CH₃CN) with 0.075% TFA in ddH₂O containing 0.1% TFA, the product fractions were pooled and lyophilized to give a white powder. The identity of **A-1** was confirmed using MALDI-TOF MS (Calcd, 2860.342; found, 2860.206).

4.4.3. Side Chain-Functionalized Fmoc-Asp(Nap)-OH (Fmoc-Dnap)

Fmoc-Asp(Nap)-OtBu: Orthogonal protected Fmoc-Asp-OtBu (2.0 g, 4.9 mmol) was dissolved in DCM (0.2 M), and subsequently 1-hydroxy-7-azabenzotriazole (HOAt, 1 equiv, 0.65 g, 4.9 mmol), 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide (EDC, 2 equiv, 1.9 g, 9.7 mmol), and DIPEA (3 equiv, 2.5 mL, 15 mmol) were added. The reaction mixture was stirred for 10 min at 0 °C followed by the addition of *N*-naphthylethylenediamine (Nap; 2 equiv, 2.5 g, 9.7 mmol) and DIPEA (2 equiv, 1.7 mL, 9.7 mmol). The reaction mixture was stirred for 20 min at 0 °C and stirring was continued at room temperature for additional 4 h. After complete disappearance of the starting material was confirmed by thin layer chromatography (TLC), the reaction mixture was diluted with DCM and subsequently washed with 1 M HCl (aq, 3x), saturated NaHCO₃ (aq, 3x), and brine (3x), dried Na₂SO₄, filtered, and concentrated in vacuo. The residue was purified using silica gel column chromatography [hexanes/ethyl acetate (EtOAc) = 2/1 → 1/1] to give the titled compound as a greenish solid (2.2 g; yield = 79%). ¹H NMR [500 MHz, CDCl₃, δ (ppm)]: 7.78 (s, 1H), 7.67 (d, *J* = 7.3 Hz, 3H), 7.46 (d, *J* = 7.4 Hz, 2H), 7.35 (s, 2H), 7.31 (t, *J* = 7.5 Hz, 2H), 7.23 (dd, *J* = 14.3, 7.2 Hz, 2H), 7.14 (d, *J* = 8.1 Hz, 1H), 6.47 (d, *J* = 7.5 Hz, 1H), 6.13 (s, 1H), 5.94 (d, *J* = 7.4 Hz, 1H), 5.22 (s, 1H), 4.41 (s, 1H), 4.22-4.31 (m, 1H), 4.21-4.14 (m, 1H), 4.06 (t, *J* = 7.0 Hz, 1H), 3.58 (d, *J* = 4.1 Hz, 2H), 3.33 (s, 2H), 2.74-2.85 (m, 1H), 2.70 (dd, *J* = 15.4, 2.5 Hz, 1H), 1.39 (s, 9H). ¹³C NMR [125 MHz, CDCl₃, δ (ppm)]: 171.1, 170.0, 156.2, 143.8, 143.2, 141.3, 134.3, 128.6, 127.7, 127.1, 126.5, 125.9, 125.2, 124.9, 123.4, 120.3, 120.0, 117.5, 103.8, 82.7, 67.2, 51.5, 47.0, 44.8, 39.0, 38.4, 27.9. HRMS: Calcd, 524.2180; Found, 524.2181.

Fmoc-Asp(Nap)-OH: Fmoc-Asp(Nap)-OtBu (1, 1.5 g, 2.6 mmol) was co-evaporated with DCM and dissolved in a solution of 30% TFA in DCM at 0 °C. The reaction mixture was allowed to warm up to room temperature for 2 h, after which the volatiles were removed in vacuo. The residue was subjected to silica gel column chromatography (hexanes/EtOAc 1/5 → 1/15) to give the titled compound as a light greenish solid (1.3 g; 93%). ¹H NMR [500 MHz, DMSO-*d*₆, δ (ppm)]: 12.73 (s, 7H), 8.18 (t, *J* =

5.7 Hz, 35H), 8.08 (d, J = 8.1 Hz, 34H), 7.88 (d, J = 7.5 Hz, 68H), 7.67-7.77 (m, 100H), 7.62 (d, J = 8.3 Hz, 30H), 7.35-7.47 (m, 136H), 7.23-7.35 (m, 103H), 7.10 (d, J = 8.1 Hz, 7H), 6.57 (t, J = 10.7 Hz, 34H), 6.21 (s, 33H), 4.43 (td, J = 8.1, 5.6 Hz, 6H), 4.26 (dd, J = 7.0, 2.6 Hz, 11H), 4.21 (dd, J = 14.3, 7.5 Hz, 8H), 3.32-3.46 (m, 37H), 3.27 (d, J = 3.8 Hz, 15H), 2.67 (d, J = 5.4 Hz, 3H), 2.64 (d, J = 5.3 Hz, 4H), 2.51-2.61 (m, 7H), 1.13-1.40 (m, 5H). ^{13}C NMR [125 MHz, DMSO- d_6 , δ (ppm)]: 173.6, 170.2, 156.3, 144.3, 144.3, 144.3, 141.2, 134.5, 128.4, 128.1, 127.6, 127.3, 126.1, 125.7, 124.5, 123.4, 121.9, 120.6, 116.0, 103.2, 66.1, 51.2, 47.1, 43.4, 38.2, 37.6. HRMS: Calcd, 580.2806; Found, 580.2811.

4.4.4. Preparation of the Samples Containing A-1

A-1 was dissolved in hexafluoroisopropanol (HFIP, 1 mM) and allowed to stand for 1 h at room temperature. The resultant solution of **A-1** was aliquoted, lyophilized, and stored at -20 °C. The obtained powder was dissolved in a mixture of DMSO/ddH₂O (1:1, v/v) to give the final concentration of 1 mM. To aid the solvation of the peptide, the mixture was vortexed for 1 min followed by sonication for 10 min at room temperature. The resultant solution was allowed to be at room temperature for specified incubation time points. During fluorescence experiments, the solution of **A-1** was stored at 4 °C.

4.4.5. Zn(II) Binding Studies of A-1

The solution of **A-1** (20 μM) and ZnCl₂ (2.0 mM) was prepared in 20 mM ammonium acetate buffer (pH 7.4) and incubated for 1 h without agitation at room temperature. The MS analysis was performed using the Q Exactive Plus Orbitrap mass spectrometer (Thermo Fisher Scientific) with an electrospray ionization (ESI) source.

4.4.6. Modeling of A-1 with and without Zn(II)

The structures of metal-free **A-1** and Zn(II)-bound **A-1** were generated with modifications of the previously reported structures of metal-free A β (PDB: 1AMC)²⁷ and Zn(II)-bound A β (PDB: 1ZE9)²⁸ by Discovery Studio Visualizer.

4.4.7. Fluorescent Measurements

A-1 (250-500 nM) and ZnCl₂ (100 μM) with and without compounds (i.e., **L2-b**, **EDTA**, natural products; 100 μM) were mixed in 10% DPBS for 10 min without agitation. The mixture was excited at 280 nm. The FRET signal of Zn(II)-treated **A-1** was recorded from 300 to 600 nm. Particularly, the emission of **A-1** at 420 nm showed > ca. 2-fold increase in the presence of ZnCl₂, relative to that of **A-1** itself. The buffer for our measurements was selected based on (i) the solubility and (ii) aggregation rate of **A-1** as well as (iii) no presence of other divalent metal ions. In addition, based on Zn(II) titration experiments, the concentration of Zn(II) for fluorescence measurements was chosen. The fluorescence intensity of **A-1** (500 nM) at 420 nm was enhanced upon titration with Zn(II) and was saturated at ca.

100 μM of Zn(II). Thus, 500 nM of **A-1** and 100 μM of Zn(II) were used for fluorescence measurements. Moreover, Zn(II) titration to **A-1** (5 μM) was conducted in order to determine the dissociation constant (K_d) of Zn(II)–**A-1**. The K_d value was determined following previously reported methods.^{36–38,46} Furthermore, the fluorescent response of **A-1** (500 nM) in the presence of Cu(II) (1 equiv to **A-1**) was monitored. Upon incubation with Cu(II), the fluorescent intensity of **A-1** was quenched.

4.4.8. Time-dependent Fluorescence Measurements

A-1 (250 nM) was dissolved in 10% DPBS and incubated with and without ZnCl₂ (100 μM) for 10 h. Fluorescence was recorded for 10 h with an interval of 5 min at room temperature.

4.4.9. Morphologies of the Aggregates of **A-1** and A β ₄₀ with and/or without Zn(II)

A-1 (2.5 μM) was incubated with ZnCl₂ (1.0 mM) in 10% DPBS at room temperature for 10 h without agitation. In addition, A β ₄₀ (20 μM) was incubated with and without ZnCl₂ (20 μM) in a buffered solution (20 mM HEPES, pH 7.4, 150 mM NaCl) at 37 °C for 10 h with constant agitation. The samples for TEM were prepared according to previously reported methods.^{30,31} Glow-discharged grids (Formvar/Carbon 300-mesh, Electron Microscopy Sciences, Hatfield, PA, USA) were treated with the samples from different incubation time points [1, 2, 3, 4, 5, 6, 7, 8, 9, and 10 h for Zn(II)-treated **A-1** (10 μL); 0.5, 3, 5, 7, and 10 h for metal-free A β ₄₀ and Zn(II)-added A β ₄₀ (5 μL)] for 2 min at room temperature. Excess sample was removed with filter paper and washed with ddH₂O. Each grid was treated with uranyl acetate (1% w/v ddH₂O; 5 μL) for 1 min. Excess stain was blotted off and the grids were air dried for at least 20 min at room temperature. Images from each sample were taken at 200 kV with 25,000x magnification [UCRF, Ulsan, Republic of Korea (for Zn(II)-treated **A-1** samples)] and 29,000x magnification [KARA, Daejeon Republic of Korea (for the samples of metal-free and Zn(II)-bound A β ₄₀)].

4.4.10. Thioflavin-T (ThT) Assay

The kinetics of the formation of β -sheet-rich A β ₄₀ aggregates were monitored by the ThT assay according to previous reported methods.^{47,48} Each A β ₄₀ sample (20 μM) was obtained after different incubation time points (up to 12 h) at 37 °C with constant agitation (in 20 mM HEPES, pH 7.4, 150 mM NaCl) followed by treatment with ThT (20 μM). After 20 min incubation, the fluorescence intensity of ThT (λ_{ex} = 440 nm; λ_{em} = 490 nm) was measured using a microplate reader, and normalized compared to that of 12 h incubated metal-free A β ₄₀ samples.

4.4.11. Absorption Spectra of Inhibitors

The solutions of the inhibitors, i.e., **EDTA**, **L2-b**, **7**, **9**, **48**, **61**, **73**, **84**, **106**, and **139** (100 μ M; 2% v/v DMSO), were prepared in 10% DPBS. Absorption spectra of the inhibitors with and without ZnCl_2 (100 μ M) were obtained by a microplate reader at room temperature.

4.4.12. Analysis of the Covalent Bond Formation between $\text{A}\beta_{28}$ and the Inhibitor (**61**)

$\text{A}\beta_{28}$ (20 μ M) was incubated with **61** (100 μ M; 2% v/v DMSO; containing an α,β -unsaturated carbonyl group) in 20 mM ammonium acetate (pH 7.4) for 2 h at room temperature without agitation. The incubated samples were injected into the MicroTOF-QII Hybrid Quadrupole-Time of Flight mass spectrometer (Bruker, Billerica, Massachusetts, USA) equipped with an ESI source (KARA, KAIST, Republic of Korea).

4.4.13. Cell Studies

The human neuroblastoma SH-SY5Y (5Y) cell line was purchased from the American Type Culture Collection (ATCC, Manassas, VA, USA). The cell line was maintained in media containing 50% minimum essential medium (MEM) and 50% F12 (GIBCO), and supplemented with 10% fetal bovine serum (Sigma-Aldrich) and 100 U/mL penicillin (GIBCO). Cells were grown and maintained at 37 $^{\circ}\text{C}$ in a humidified atmosphere with 5% CO_2 . The cell culture used in this work did not indicate mycoplasma contamination. Cell viability upon treatment with compounds was determined by the MTT assay [MTT = 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide]. Cells were seeded in a 96 well plate (15,000 cells in 100 μ L per well). Cells were treated with pre-incubated samples containing Zn(II) and/or $\text{A}\beta$ for 1 h at room temperature without agitation followed by addition of the selected natural products. After 24 h incubation, MTT [25 μ L of 5 mg/mL in PBS (pH 7.4, GIBCO)] was added to each well and the plate was incubated for 4 h at 37 $^{\circ}\text{C}$. Formazan produced by cells was solubilized using an acidic solution of *N,N*-dimethylformamide (DMF, pH 4.5, 50% v/v, aq) and sodium dodecyl sulfate (SDS, 20% w/v) overnight at room temperature in the dark. The absorbance was measured at 600 nm by a microplate reader. Cell viability was calculated relative to that of the cells containing a volume of ddH_2O (containing 1% DMSO) equal to the volume of protein sample added.

4.4.14. Statistical Analysis

All data present mean \pm standard error of the mean (S.E.M.). For comparisons between two groups, Student's two-tailed unpaired *t* test was employed. Statistical difference was considered significant at $*P < 0.05$.

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Publications

1. **Juhye Kang**,[†] Jung Seung Nam,[†] Hyuck Jin Lee, Geewoo Nam, Hyun-Woo Rhee, Tae-Hyuk Kwon, and Mi Hee Lim. "Chemical Strategies to Modify Amyloidogenic Peptides by Iridium(III) Complexes: Coordination and Photo-induced Oxidation" *In Revision* ([†]Co-first authorship).

2. Geewoo Nam, Yonghwan Ji, HyuckJin Lee, **Juhye Kang**, Yelim Yi, Mingeun Kim, and Mi Hee Lim. "Orobol: An Isoflavone with Regulatory Multifunctionality against Four Pathological Factors of Alzheimer's Disease" *Submitted*.
 3. Yuxi Lin, Bikash Sahoo, Daisaku Ozawa, Misaki Kinoshita, **Juhye Kang**, Mi Hee Lim, Masaki Okumura, Sihyun Ham, Hyung-Sik Won, Kyoung-Seok Ryu, Toshihiko Sugiki, Toshimichi Fujiwara, Ayyalusamy Ramamoorthy, Young-Ho Lee. "Diverse Structural Conversion and Aggregation Pathways of Alzheimer's Amyloid- β (1-40)" *In Revision*.
 4. Misun Lee, Min Hee Park, Ju Youn Lee, Min Seock Jeong, Kang Ho Park, Seung Hoon Han, Geewoo Nam, Mingeun Kim, **Juhye Kang**, Eunyoung Tak, Min Sun Kim, Joo-Yong Lee, Hee Kyung Jin, Jae-Sung Bae, Mi Hee Lim. "A Compact Molecular Entity Improving Cognitive Function by Restoring the Phagocytic Aptitude of Microglia" *Submitted*.
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 6. Hyuck Jin Lee,[†] Young Geun Lee,[†] **Juhye Kang**,[†] Seung Hyun Yang, Ju Hwan Kim, Amar B.T. Ghisaidoobe, Hyo Jin Kang, Sang-Rae Lee, Mi Hee Lim, and Sang J. Chung. "Monitoring Metal-Amyloid- β Complexation by a FRET-based Probe: Design, Detection, and Inhibitor Screening" *Chemical Science*, **2019**, *10*, 1000-1007 ([†]Co-first authorship).
- *Selected as "2018 Chemical Science HOT Article Collection" and featured as the "Back cover".
7. Jong-Min Suh, Gunhee Kim, **Juhye Kang**, Mi Hee Lim. "Strategies Employing Transition Metal Complexes to Modulate Amyloid- β Aggregation" *Inorganic Chemistry*, **2019**, *58*, 8-17.
 8. Masha G. Savelieff,[†] Geewoo Nam,[†] **Juhye Kang**,[†] Hyuck Jin Lee, Misun Lee, and Mi Hee Lim. "Development of Multifunctional Molecules as Potential Therapeutic Candidates for Alzheimer's Disease, Parkinson's Disease, and Amyotrophic Lateral Sclerosis in the Last Decade" *Chemical Reviews*, **2019**, *119*, 1221-1322 ([†]Co-first authorship).
 9. Hyuck Jin Lee, Masha G. Savelieff, **Juhye Kang**, Megan Brunjes Brophy, Toshiki G. Nakashige, Shin Jung C. Lee, Elizabeth M. Nolan, and Mi Hee Lim. "Calprotectin Influences the Aggregation of Metal-free and Metal-bound Amyloid- β by Direct Interaction" *Metallomics*, **2018**, *10*, 1116-1127.
 10. Eunju Nam, Jeffrey S. Derrick, Seunghee Lee, **Juhye Kang**, Jiyeon Han, Shin Jung C. Lee, Su Wol Chung, and Mi Hee Lim. "Regulatory Activities of Dopamine and Its Derivatives toward Metal-free and Metal-induced Amyloid- β Aggregation, Oxidative Stress, and Inflammation in Alzheimer's Disease" *ACS Chemical Neuroscience*, **2018**, *9*, 2655-2666.

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14. **Juhye Kang**,[†] Shin Jung C. Lee,[†] Jung Seung Nam,[†] Hyuck Jin Lee, Myeong-Gyun Kang, Kyle J. Korshavn, Hyun-Tak Kim, Jaeheung Cho, Ayyalusamy Ramamoorthy, Hyun-Woo Rhee, Tae-Hyuk Kwon, and Mi Hee Lim. “An Iridium(III) Complex as a Photoactivatable Tool for Oxidation of Amyloidogenic Peptides with Subsequent Modulation of Peptide Aggregation” *Chemistry - A European Journal*, **2017**, 23, 1645-1653 ([†]Co-first authorship).

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17. Hyuck Jin Lee, Richard A. Kerr, Kyle J. Korshavn, Jiyeon Lee, **Juhye Kang**, Ayyalusamy Ramamoorthy, Brandon T. Ruotolo, and Mi Hee Lim. “Effects of Hydroxyl Group Variations on a Flavonoid Backbone toward Modulation of Metal-free and Metal-induced Amyloid- β Aggregation” *Inorganic Chemistry Frontiers*, **2016**, 3, 381-392.
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25. In Hong Hwang, Young Dan Jo, Ha-Yeong Kim, **Juhye Kang**, Jin Young Noh, Min Young Hyun, Cheal Kim, Youngmee Kim, and Sung-Jin Kim. "Novel Mn^{II} Coordination Compounds Constructed from Benzoate and Various Bipyridyl Ligands: Magnetic Property and Catalytic Activity" *Polyhedron*, **2012**, 42, 282-290.
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Patents

1. Tae-Hyuk Kwon, Hyun-Woo Rhee, Mi Hee Lim, Jung Seung Nam, **Juhye Kang**, Myeong-Gyun Kang, and Hyun-Tak Kim. "Pharmaceutical Composition for Anticancer Containing Cyclometalated Transition Metal Complex" *Korean Pat. Appl. Publ.* **2017**, 10-1743594.
2. Cheal Kim, Eun Joo Song, **Juhye Kang**, Ga Rim You, and Myoung Mi Lee. "Quinoline Compounds, Agent Selecting Zinc Ion, Cadmium Ion and Copper Ion Using the Same, Detecting Method and Detecting Device Thereof" *Korean Pat. Appl. Publ.* **2016**, 10-1638682.

Presentations

1. **Juhye Kang**, Shin Jung C. Lee, Jung Seung Nam, Hyuck Jin Lee, Kyle J. Korshavn, Hyun-Tak Kim, Jaeheung Cho, Ayyalusamy Ramamoorthy, Hyun-Woo Rhee, Tae-Hyuk Kwon, and Mi Hee Lim. Poster Slam & Presentation. “An Iridium(III) Complex as a Photoactivatable Tool for Oxidation of Amyloidogenic Peptides with Subsequent Modulation of Peptide Aggregation” *The 4th International Symposium for Molecular Neurodegenerative Disease Research*, **2018**.
2. **Juhye Kang**, Shin Jung C. Lee, Jung Seung Nam, Hyuck Jin Lee, Myeong-Gyun Kang, Kyle J. Korshavn, Hyun-Tak Kim, Jaeheung Cho, Ayyalusamy Ramamoorthy, Hyun-Woo Rhee, Tae-Hyuk Kwon, and Mi Hee Lim. “An Iridium(III) Complex as a Photoactivatable Tool for Oxidation of Amyloidogenic Peptides with Subsequent Modulation of Peptide Aggregation” *International Union of Materials Research Societies – International Conference on Electronic Materials 2018 (IUMRS-ICEM 2018)*, **2018**.
3. **Juhye Kang** and Mi Hee Lim. Oral Presentation. “Iridium(III) Complexes as Modulators for Amyloid- β Aggregation through Multiple Mechanisms” *Symposium on Chemistry and Life*, **2018**.
4. Hyuck Jin Lee, Young Geun Lee, **Juhye Kang**, Seung Hyun Yang, Ju Hwan Kim, Amar B.T. Ghisaidoobe, Hyo Jin Kang, Sang-Rae Lee, Mi Hee Lim, and Sang J. Chung. “FRET-based Method for the Real-time Identification of Metal–Amyloid- β Interaction: Rational Design, Detection, and Inhibitor Screening” *The Bioinorganic Chemistry Symposium*, **2018**.
5. **Juhye Kang** and Mi Hee Lim. Oral & Poster Presentations. “Iridium(III) Complexes as Modulators for Amyloid- β Aggregation through Multiple Mechanisms” *The Bioinorganic Chemistry Symposium*, **2017**.
*Awarded as a “Grand Prize for Poster Award”.
6. **Juhye Kang**, Shin Jung C. Lee, Jung Seung Nam, Hyuck Jin Lee, Myeong-Gyun Kang, Kyle J. Korshavn, Hyun-Tak Kim, Jaeheung Cho, Ayyalusamy Ramamoorthy, Hyun-Woo Rhee, Tae-Hyuk Kwon, and Mi Hee Lim. “An Iridium(III) Complex as a Photoactivatable Tool for Oxidation of Amyloidogenic Peptides with Subsequent Modulation of Peptide Aggregation” *The 8th Asian Biological Inorganic Chemistry Conference*, **2016**.
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8. **Juhye Kang**, Jung Seung Nam, Shin Jung C. Lee, Hyuck Jin Lee, Hyuntak Kim, Hyun-Woo Rhee, Tae-Hyuk Kwon, and Mi Hee Lim. Poster Slam & Presentation. “Modulation of Amyloid- β Aggregation Pathways by Iridium(III) Complexes through Three Distinct

Mechanisms” *The 116th National Meeting of the Korean Chemical Society*, **2015**.

9. **Juhye Kang**, Hyuck Jin Lee, Shin Jung C. Lee, and Mi Hee Lim. “Modulation of Amyloid- β Aggregation Pathways by Iridium(III) Complexes” *The Bioinorganic Chemistry Symposium*, **2015**.
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